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GenCore version 5.1.6
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- protein search, using sw model OM protein 3, 2005, 09:45:35 ; Search time 39 Seconds June Run on:

(without alignments) 86.348 Million cell updates/sec

US-10-792-311-1 Title: Perfect score:

166 1 AKKYAKKEKAAKKAYKKEAKAKAABAAAKEAAYEA 35 Sequence:

BLOSUM62 Scoring table:

283416 seqs, 96216763 residues Gapop 10.0 , Gapext 0.5 Searched:

7756 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 35

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	nonhistone chr	protamine S4 - sma	epsilon receptor m	ribosomal protein	antifreeze protein	antifreeze protein	metalloproteinase	sperm-specific pro	neurofilament trip	hypothetical prote	' ⊏	cAMP response elem	neurofilament heav	internal peptide V	hypothetical prote	histone H3 - mouse	hypothetical prote	•	kinetoplast DNA-as	lysine-rich 18K pr	Hu-like protein HB	ribosomal protein	histone H2A.Z - ra	photosystem I chai	ribosomal protein	hypothetical prote	protein-tyrosine k	hypothetical prote	
SUMMARIES																														
SUMM	a	131	A41270	A61220	S51071	A05162	FDF15G	T43163	B45316	802571	H95021	B97032	PD0014	153671	B04348	E64577	A39525	AE0612	A05112	D47256	A56753	A43768	T44245	A27074	S06149	S11416	AC0717	A49955	13	E70202
	DB		7	7	7	~	Н	~	N	~	~	~	~	~	N	~	7	7	7	~	7	7	7	~	~	7	~	~	~	7
	& Query Match Length	33	32	18	25	33	33	33	32	30	30	34	30	20	23	30	35	35	35	22	24	27	29	32	20	20	29	30	30	31
	Query Match		25.0	24.1	23.5	23.5	22.9	21.7	21.7	21.4	21.1	21.1	20.8	20.5	20.5	20.5	20.5	20.5	20.2	19.9	19.9	19.9	19.9	19.9	19.3	19.3	19.3	19.3	19.3	19.3
	Score		41.5	40		39	38	36	36	35.5	35	35	34.5	34	34		34	34	33.5	33	33	33	33	33	32	32	32	32	32	32
	Result No.	1	7	e	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

cytochrome c552 - ubiquitin / riboso photosystem I chai histone H2B - huma photosystem I 16.1 chromogranin-B - r GTP-binding regula ribosomal protein transforming prote gaegurin 3 - Korea ribosomal protein	photosystem 118.5 photosystem 118.5 ribosomal protein 24K antigen - Myco internal peptide V
A48366 B40186 S00315 B33239 PQ0683 F49164 I54247 S71226 PC2302 S51069	PQ0692 A28144 B60248 A04348
000000000000	0000
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	112 116 23
19.0 18.7 18.7 18.7 18.7 18.7 18.7	18.11.11.11.11.11.11.11.11.11.11.11.11.1
31.5 31.5 31.5 31 31 31 31 31 30.5	0000
	1 4 4 4 4 1 62 62 4 72

ALIGNMENTS

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C, Accession: A6110
R, Walker, J. M.; Goodwin, G. H.; Johns, E. W.
Int. J. Pept. Protein Res. 11, 301-304, 1978
A; Title: The amino terminal sequence of high mobility group non-histone chromosomal prote
A; Tetles: The amino terminal sequence of high mobility group non-histone chromosomal prote
A; Reference number: A61310; MUID:78217501; PMID:669887
A; Status: preliminary
A; Status: preliminary
A; Residues: 1-33 *Wal.>
A; Cross-reference: UNIPROT:Q7M2Y3
C; Superfamily: nonhistone chromosomal protein HMG-17
C; Keywords: chromosomal protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protentine S4 - smaller spotted catshark

NyAlternate names: scylliorhinine S4

NyAlternate names: scylliorhinine S4

C)species: Scylliorhinus canicula (smaller spotted catshark, smaller spotted dogfish)

C)Bacise: 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 09-Jul-2004

C)Accession: A41270; S12285

R;Sautiere, P; Gusse, M; Briand, G; Martinage, A; Chevaillier, P.

B;ochim. Biophys. Acta 791, 82-86, 1984

A;Title: Primary structure of scylliorhinine S4, a protamine isolated from sperm nuclei c

A;Reference number: A41270

A;Reference number: Drotein

A;Residues: 1-32 cSAU>

A;Residues: 1-32 cSAU>

A;Residues: Cata Taylor Sautiere, P; Chauviere, M; Chevaillier, P.

Biochim. Biophys. Acta 748, 93-98, 1983

A;Title: Extraction, purification and characterization of the sperm protamines of the docyntherence number: S01463; MUID:84000513; PMID:6615852

A;Residues: 1-55 cGUS>

C;Keywords: DNA binding; sperm; testis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
nonhistone chromosomal protein HMG-14 - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 09-Jul-2004
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Gaps

5

Length 33;

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C;Species: Listeria ivanovii
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43163
R;Gouin, E.; Dehoux, P.; Mengaud, J.; Kocks, C.; Cossart, P.
Infect. Immun. 63, 2729-2737, 1995
A;Title: IactA of Listeria ivanovii, although distantly related to Listeria monocytogenes
A;Reference number: 222322; MUID:95310034; PMID:7790091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Richardpartty, A.; Hew, C.L.; Shears, M.; Fletcher, G.
Can. J. Zool. 66, 403-408, 1988
A;Title: Primary structures of the alanine-rich antifreeze polypeptides from grubby sculf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Cross-references: UNIPROT:Q48578; EMBL:U19035; NID:g687659; PID:g687661; PIDN:AAA80583.
A,Experimental source: strain CLIP 257
                                                                                                                                                                                                                                                                                                                                                                                                 antifreeze protein GS-5 - grubby sculpin
C;Species: Myoxocephalus aenaeus (grubby sculpin)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sperm-specific protamine-like protein - California mussel (fragment)
N;Alternate names: phil; PL-III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Superfamily: zinc metalloendopeptidase, neutral protease type
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 38; DB 1; Length 33;
Pred. No. 7.2e+02;
1; Mismatches 12; Indels
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                                                                                                          Score 39; DB 2;
Pred. No. 5.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     metalloproteinase - Listeria ivanovii (fragment)
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C;Superfamily: antifreeze protein
C;Keywords: antifreeze; blocked amino end
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A,Cross-references: UNIPROT:P04367
C,Superfamily: antifreeze protein
C,Keywords: antifreeze
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                                                                                                          Query Match 23.5%;
Best Local Similarity 50.0%;
Matches 15; Conservative
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Best Local Similarity 48.09
Watches 12; Conservative
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nes 7; Conservative
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Eur. J. Blochem. 226, 169-177, 1994
A;Title: Purification and characterization of the 30S ribosomal proteins from the bacter
A;Reference number: S51053; MUID:95045586; PMID:7957245
A;Accession: S51071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: protein
A;Residues: 1-18 <MAT>
A;Cross-treferences: UNIPROT:Q7M060
C;Comment: This serine proteinase from a T cell hybridoma does not reduce levels of CD23
C;Keywords: hydrolase; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                 R;Matsushita, S.; Katz, D.H.
Cell. Immunol. 137, 252-259, 1991
A;Title: The murine epsilon receptor modulating protein: a novel serine protease which
A;Reference number: A61220, MUID:91356570, PMID:1679381
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C;Species: Myoxocephalus scorpius (shorthorn sculpin, daddy sculpin)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                       epsilon receptor modulating protein (EC 3.4.21.-) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ribosomal protein S20 - Thermus aquaticus (fragment)
C;Species: Thermus aquaticus
C;Date: 15-Jul-1995 #sequence_revision 01-Nov-1996 #text_change 01-Nov-1996
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R;Hew, C;L:; Joshi, S.; Wang, N.C.; Kao, M.H.; Ananthanarayanan, V.S.
Eur. J Biochem. 151, 167-172, 1985
A;Title: Structures of shorthorn sculpin antifreeze polypeptides.
A;Reference number: A91150; MUID:85285003; PMID:4029130
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     DB 2; Length 32;
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                                                         Indels
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A;Residues: 1-25 <TSI>
A;Note: the source is designated as Thermus thermophilus
C;Keywords: protein biosynthesis; ribosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; L
2.7e+02;
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42.9%; Pred. No. 4.5e+02;
25.0%; Score 41.5; DB 2
llarity 37.9%; Pred. No. 3e+02;
Conservative 5; Mismatches 1
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; Pred. No. 2.7e4
2; Mismatches
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Best Local Similarity 60.09
Matches 12; Conservative
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A; Molecule type: protein
A; Residues: 1-33 <HEW>
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nes 9, Conserv
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Matches 11; Conserv
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     Query Match
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Matches
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Gaps

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CAMP response element-binding protein 11.2K, 16K - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Species: L0-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 09-Jul-2004

C;Accession: P00014

R;Lee, M.Y.; Hwang, E.S.; Lee, S.K.
Biochen: Biophys. Res. Commun. 246, 50-54, 1998

A;Title: Novel CRE-binding proteins of 11-16 kDa bind to the LDH A-gene CRE in a sequence A;Reference number: P00013; MUID:98262915; PMID:9600066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Cross-references: UNIPROT:097K50; GB:AE001437; PIDN:AAK79045.1; PID:g15023984; GSPDB:GP. A,Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clos
A,Reference number: A96900, MUID:21359325, PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C,Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: B97032
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, J.; Daly, M.J.; Bennett, G.N.; Koonin, B.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transcription regulator, AcrR family [imported] - Clostridium acetobutylicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neurofilament heavy subunit - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: IS3671
G;R;Figlewicz, D.A; Rouleau, G.A.; Krizus, A.; Julien, J.P.
Gene 132, 297-300, 1993
                                                                                                                              Gaps
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46.2%; Pred. No. 1.5e+03;
tive 1; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.1%; Score 35; DB 2; 1
31.8%; Pred. No. 1.5e+03;
iive 6; Mismatches 9;
                                                   Score 35; DB 2; ]
Pred. No. 1.4e+03;
                                                                                                                              1; Mismatches
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A;Residues: 1.30 e.LES-
A;Cross-references: UNIRROT:Q7M0A0
C;Superfamily: histone H2B
                                                       21.1%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 58.3
Matches 7; Conservative
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                                                                                                                                                                                                          2 KKYAKKEKAAKK 13
                                                                                                                                                                                                                                                                                 4 KKYENDEKSOKK 15
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nes 12; Conserv
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A; Residues: 1-34 < KUR>
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A;Status: preliminary
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Matches
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Cipate: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
Cipate: District of the cipate of the cip
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                                                                                                                      Ricarlos, S.; Jutglar, L.; Borrell, I.; Hunt, D.F.; Ausio, J.
J. Biol. Chem. 268, 185-194, 1993
A.Title: Sequence and characterization of a sperm-specific histone H1-like protein of A; Reference number: A45316; MUID:93106999; PMID:7677995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C,Accession: S02571
C,Accession: S02571
R;Geisler, N.; Vandekerckhove, J.; Weber, K.
R;Geisler, N.; Vandekerckhove, J.; Weber, K.
REBS. Lett. 221, 403-407, 1987
A;Title: Location and sequence characterization of the major phosphorylation sites of A;Reference number: S02570; MUID:87304852; PMID:3114005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phosphoprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neurofilament triplet protein H - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 10-Dec-1999
C;Species: Mytilus californianus (California mussel)
C;Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: B45316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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A;Note: 5-Glu, 19-Glu, and 21-Glu were also found
C;Superfamily: neurofilament triplet H protein
C;Keywords: colled coil; heterotrimer; intermediate filament; nerve;
F;3,17/Binding site: phosphate (Ser) (covalent) #status experimental
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                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: protein
A;Residues: 1-35 <CAR>
A;Cross-references: UNIPROT:P35422
A;Note: sequence extracted from NCBI backbone (NCBIP:121400)
C;Keywords: DNA binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 AKKAYKKEA----KAKA---AEAAKEAA 32
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Best Local Similarity 56.2%;
Matches 9; Conservative 1
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A; Residues: 1-30 < KUR>
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C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Datesion: E6457
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne Son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Reference number: A64520; MUID:97394467; PMID:9252185
                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-20 <RES>
A;Cross-references: UNIPROT:Q16070; GB:S66488; NID:g452861; PIDN:AAB28609.1; PID:g452862
A;Title: Polymorphism in the multi-phosphorylation domain of the human neurofilament hea A;Reference number: 153671; MUID:94040777; PMID:8224877 A;Accession: 153671
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C;Comment: This protein is a cleavage product of P22 protein that is incorporated into
C;Superfamily: phage T4 gene 22 protein
C;Keywords: head protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: B04348; A04348 — R;Van Eerd, J.; Tsugita, A. B;Van Eerd, J.P.; Champe, S.P.; Yager, L.; Kubota, I.; Tsugita, A. J. Mol. Biol. 117, 521-524, 1977 — A;Title: Primary structure of internal peptide VII of T-even bacteriophages. A;Reference number: A92849; MUID:78111436; PMID:604510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C,Species: phage T6
C,Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                         Length 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 20.5%; Score 34; DB 2; I
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 8; Conservative 2; Mismatches 6;
                                                                                                                                                                                                                                       C,Genetics:
A,Gene: GDB:NEFH
A,Cross-references: GDB:120225; OMIM:162230
A,Map position: 22q12.1-22q13.1
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| S AKSPEKAKSPEKEEAK 20
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0747m3 geobacter s
071996 psammechinu
P88588 phyllomedus
07m2y3 sus scroids
083175 cauliflower
P80259 scyliorhinu
08p382 xanthomonas
07m060 mus musculu
09p4m2 trypanosoma
P83420 oiketicus k
P04367 myoxocephal
P83420 oiketicus k
P04367 myoxocephal
P8362 cupiennius
07rc19 plasmodium
P8355 rattus norv
P83561 cupiennius
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Q7RJZ2
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2: uniprot_trembl:*
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VG22_BPT6 063726 025208 025208 029EL7 0945D4 084EB11 086VY8 091CC6 091CC6 091CC6 091CC6 091CC6 091CC6	PRT; 35 AA. 7, Created) 7, Last sequence upda 7, Last annotation up; 126/science.1088727; 126/science.1088727; 14 M., Ward N.L., Bean Daugherty S.C., DeBoy Sallivan S.C., DeBoy	Putite O., Tran B., Rome Feldblyum T.V., Utter Fraser C.M.; Fraser C.M
20.5 20.5 20.5 20.5 20.5 20.5 20.5 20.5	PRELIMINARY; (TEMBLEEL 2 (TEM	Davidsen T.W., Zafar N., White O., Traweldsen T.W., Zafar N., White O., Traweldsen T.W., Zafar N., White O., Traweldsen S.E., Lovley D.R., Praser C.M "Genome of Geobacter sulfurreducens: menvironments."; Science 302:1967-1969(2003). EMBL, ARG017180; ARR36633.1; TIGR; GSU3242;
33 33 33 33 33 33 33 33 33 33 33 33 33	TLT 1 Q747M3 Q747M3 Q747M3 G5-JUL-2004 (TEM 05-JUL-2004 (TEM 05-JUL-2004 (TEM 05-JUL-2004 (TEM Hypothetical prot OrderediocusNames Geobacter sulfurz Bacteria, Proteob Geobacteraceae; G NCBI_TAXID=3554; SEQUENCE FROM N.A STRAIN=PCA / ATCC PUMPGG-14671304; Methe B.A., Nelso Heidelberg J.F., Methe B.A., Nelso Heidelberg J.F., Medun M.I., Kolon Gwinn M.I., Kolon	Davidsen T.M., Zafar N. Weidman J.F., Khouri H. Van Aken S.E., Lovley D. Genome of Geobacter su environments "; Science 302:1967-1969(2 EMBL, AE017180; ARR3663 TIGR; GSU3242;Complete proteome; Hypo SEQUENCE 35 AA, 3966 Query Match Encal Similarity 55 Matches 16; Conservativy 2 KKYAKKEKAAKKAY [
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33 AA.

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01-MAR.2004 (TrEMBLrel. 26, Created)
01-MAR.2004 (TrEMBLrel. 26, Last sequence update)
01-MAR.2004 (TrEMBLrel. 26, Last annotation update)
Nonhistone chromosomal protein HWG-14 (Fragment).
Sus scrofa domestica (domestic plg).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -I. FUNCTION: Antibacterial activity against Gram-positive bacterium S.aureus and B.faecalis, and Gram-negative bacterium P.aeruginosa and E.coli. Has antiprotozoal activity against T.cruzi.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Skin.
-!- MASS SPECIFOMETRY: MM=3154.0; METHOD=Electrospray; RANGE=1-33; NOTE=Ref.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99404773; PubMed=10477123; DOI=10.1016/S0196-9781(99)00050-9; Batista C.V.F., da Silva L.R., Sebben A., Scaloni A., Ferrara L., Paiva G.R., Olamendi-Portugal T., Possani L.D., Bloch C. Jr.; "Antimicrobial peptides from the Brazilian frog Phyllomedusa
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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MEDLINE=22370988; PubMed=12379643; DOI=10.1074/jbc.M209289200;
Brand G.D., Leite J.R.S.A., Silva L.P., Albuquerque S., Prates M.V.,
Azevedo R.B., Carregaro V., Silva J.S., Sa V.C.L., Brandao R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Dermaseptins from Phyllomedusa oreades and Phyllomedusa distincta. Anti-Trypanosoma cruzi activity without cytotoxicity to mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, MASS SPECTROMETRY, CIRCULAR DICHROISM ANALYSIS, AND SYNTHESIS.
                                  MEDLINE=79001915; PubMed=688387; DOI=10.1016/0092-8674(78)90249-0; Schaffner W., Kunz G., Daetwyler H., Telford J., Smith H.O., Birnstiel M.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Phyllomedusa distincta (Monkey frog).
Bukaryota; Metacota; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
Phyllomedusinae; Phyllomedusa.
                                                                                                                      "Genes and spacers of cloned sea urchin histone DNA analyzed by sequencing."; Cell 14:655-671(1978). EMBL; J01184; AAB59209.1; -.
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0
                                                                                                                                                                                                                                                                                                                        Query Match 27.7%; Score 46; DB 2; Length 22; Best Local Similarity 57.1%; Pred. No. 3.4e+02; Matches 12; Conservative 1; Mismatches 8; Indels
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46.9%; Pred. No. 6.2e+02;
tive 4; Mismatches 11;
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les 15; Conserv
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                          SEQUENCE FROM N.A.
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WEDLINE=78217501; PubMed=669887;
Walker J.M., Goodwin G.H., Johns E.W.;
Walker J.M., Goodwin G.H., Johns E.W.;
With amino terminal sequence of high mobility group non-histone chromosomal protein HMG 14, showing sequence homologies with two other chromosomal protein HMG 14, showing sequence homologies with two other in the J. Pept. Protein Res. 11:301-304(1978).

Int. J. Pept. Protein Res. 11:301-304(1978).

R GO; GO:0000785; C:chromatin; IEA.

R GO; GO:0005634; C:nucleus; IEA.

R GO; GO:0005677; F:DNA binding; IEA.

R GO; GO:0005677; F:DNA binding; IEA.

R PRINTS; PRO0925; HMG 14_17.

R PRINTS; PRO0925; HMG14_17; 1.
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26.5%; Score 44; DB 2; Length 33;
Best Local Similarity 38.5%; Pred. No. 7.9e+02;
Matches 10; Conservative 7; Mismatches 9; Indels
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Coat protein, partial cds. (Fragment).
Cauliflower mosaic virus.
Viruses; Retroid viruses; Caulimoviridae; Caulimovirus.
NCBI_TAXID=10641;
                                                                                                                                                                                                                                                                                                                                 33 AA; 3531 MW; 9EC7492EA8CAEA2B CRC64;
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GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0005198; F:structural molecule activity; IEA
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MEDLINE=90320145; PubMed=2371775;
Vaden V.R., Melcher U.K.;
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nes 10; Conservative
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C STRAIN=ATCC 33913 / NCPPB 528;

X MEDLINE=2202145; PubMed=12024217; DOI=10.1038/417459a;

A Gasjiva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

A Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

A Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

A Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

A Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

A Cicarelli R.M.B., Couttinho L.L., Cursinno-Santos J.R., Bl-Dorry H.,

Raria J.B., Ferreira A.J.S., Ferreira R.C.C., Gruber A.,

Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Gruber A.,

Ratsuyama A.M., Kishi L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F.,

Locall B.C., Machado M.A., Madeira A.M. Myarki C.Y., Moon D.H.,

Martins B.C., Meidanis J., Monck C.F.M., Myarki C.Y., Moon D.H.,

Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                   Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Blasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
Scyliorhinidae; Scyliorhinus.
                                                                                                                                                                                                                                                                                                                                                               PIR; A41270; A41270.
Chromosomal protein; Direct protein sequencing; DNA condensation;
DNA-binding; Nuclear protein; Nucleosome core; Spermatogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      25.0%; Score 41.5; DB 1; Length 32; 37.9%; Pred. No. 1.4e+03; Ative 5; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 32 AA; 3882 MW; 4C4E9F58958D1AEF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein XCC4196.
                                                                                                        01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                   32 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 KKYAKKEKAAKKAYKKEAKAKAAEAAKE 30
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                      7 KKYHKRYKKKYKVYKPYKKKK 27
 KKYAKKEKAAKKAYKKEAKAK
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                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                     NCBI_TaxID=7830;
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                                                                                                                                                                                                                                            TISSUE=Testis;
                                                                                                                                            Protamine S4.
                                                                                PRT4 SCYCA P30259;
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                                                                        PRT4_SCYCA
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Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F., Spinola L.A.F., Takita M.A., Tamura R.B., Teixeira B.C., Tezza R.I.D., Trindade Gos Santos M., Truffi D., Tsai S.M., White F.F., Setubal J.C., Kitajima J.P., Comparison of the genomes of two Xanthomonas pathogens with differing Nature 417,459-463 (2002).

EMBL, AR012546; AAM43412.1; -. Complete proteome. 32 AA; 3674 MW; 72C4849D4149F3EA CRC64;
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Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5693;
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Unanbiguous identification of histone H1 in Trypanosoma cruzi.";
J. Call. Biochem. 52:431-439 (1993).
SEQUENCE 17 AA; 1820 MW; AD19BCC52D8ECCD5 CRC64;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=91356570; PubMed=1679381;
Matsushita S., Katz D.H.;
"The murine epsilon receptor modulating protein: a novel serine protease which modulates CD23 binding of IgE.";
Cell. Immunol. 137:252-259(1991).
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Epsilon receptor modulating protein (EC 3.4.21.-) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24.1%; Score 40; DB 2; Length 18; 60.0%; Pred. No. 1.2e+03;
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                                                                                                                                                                                                                                                                                                                            24.7%; Score 41; DB 2; Length 32; 48.0%; Pred. No. 1.6e+03; ive 2; Mismatches 7; Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 26, Created)
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Gaps

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12; Indels

1; Mismatches

Score 39; DB 1; Length 33; Pred. No. 2.6e+03;

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MEDLINE=96223980; PubMed=8626748; DOI=10.1074/jbc.271.8.4106; OGD Z., Ewart K.V., Hu Z., Fletcher G.L., Hew C.-L.; Ewart K.V., Hu Z., Fletcher G.L., Hew C.-L.; Skin antifreeze protein genes of the winter flounder, Pleuronect americanus, encode distinct and active polypeptides without the secretory signal and prosequences."; Biol. Chem. 271:4106-4112(1996).

- FUNCTION: Antifreeze proteins lower the blood freezing point.-I SIMILARITY: Belongs to the type-I APP family.
                                                                                                                                     PIR; A05162, A05162.
Antifreeze protein; Direct protein sequencing; Repeat.
SEQUENCE 33 AA; 2939 WW; 8B74CC4C06A1208A CRC64;
                                                                                                                                                                                          23.5%;
50.0%;
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hes 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                           (Fragment).
                                                                                                                                                                                                       Local Similarity
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NCBI_TaxID=8096;
                                                                                                                                                                                                                                                                                                                                                                                                           Histone 1.1
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    [2]
SEQUENCE.
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--- FUNCTION: Cecropins have lytic and antibacterial activity against several Gram-positive and Gram-negative bacteria. Has also activity against fungi.
--- SUBUNIT: Monomer.
                                                                                                                                                                                                                                                                                                 SEQUENCE, FUNCTION, SUBUNIT, SUBCELLULAR LOCATION, TISSUE SPECIFICITY
                  Gaps
                                                                                                                                                                                                                              Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Tineoidea;
Psychidae; Oiketicinae; Oiketicus.
NCBI_TaxID=201386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
Cottoidei; Cottidae; Myoxocephalus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDINE=85285003; PubMed=4029130;
Mew C.-L., Joshi S., Wang N.-C., Kao M.H., Ananthanarayanan V.S.;
"Structures of shorthorn sculpin antifreeze polypeptides.";
Eur. J. Blochem. 151:167-172(1985).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibiotic; Direct protein sequencing; Fungicide; Hemolymph;
                                                                                                                                                                                                                                                                                                                                                                                                                   -i- SUBCELLULAR LOCATION: Secreted.
-i- TISSUE SPECIFICITY: Hemolymph.
-i- MASS SPECTROMETRY: MW=3818.89; METHOD=MALDI; RANGE=1-?;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Myoxocephalus scorpius (Shorthorn sculpin) (Daddy sculpin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.5%; Score 39; DB 1; Length 32; 36.7%; Pred. No. 2.6e+03; tive 4; Mismatches 15; Indels
                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 32
32 AA; 3434 MW; F6942D09A7BDC1F0 CRC64;
60.0%; Pred. No. 1.4e+03;
tive 1; Mismatches 5;
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1- SIMILARITY: Belongs to the cecropin family.

InterPro; IPR000875; Cecropin.

Pfam; PF00272; Cecropin; 1.

PROSITE; PS00268; CECROPIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-MAR-1987 (Rel. 04, Created)
20-MAR-1987 (Rel. 04, Last sequence update)
20-UUL-2004 (Rel. 44, Last annotation update)
Antifreeze peptide SS-3.
                                                                                                                                                                           28-FEB-2003 (Rel. 41, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                     32 AA.
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                                                                                                                                                                                                     Cecropin (Fragment).
Oiketicus kirbyi (Bagworm moth).
                                                                                                                                                                28-FEB-2003 (Rel. 41, Created)
                                           22
                                                         3 KKAPKKAVKKAPKKK 17
                Conservative
                                         EKAAKKAYKKEAKAK
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  Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Insect immunity.
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P04367;
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P83420;
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SEQUENCE
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Matches
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Trypanosoma brucēi.
Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5691;
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Can. J. Zool. 66:403-408(1988).
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01-FEB-1991 (Rel. 17, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Antifreeze peptide GS-5.
Myoxocephalus aenaeus (Grubby sculpin).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Teleostei; Buteleostei; Neoteleostomi;
Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
Cottodei; Cottidae; Myoxocephalus.
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Last annotation update)
                                                                                                                                                                                                                           20 AA.
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5 AKKEKAAKKAYKKEAKAK--AAEAAKEAA 32
                           3 APARAAAKTAADALAAAKTAADAAAAAA 32
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Job time : 173 secs
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"Characterisation of antibacterial activity of peptides isolated from the venom of the spider Cupiennius salei (Araneae: Ctenidae).";

Toxicon 38:373-380(2000).

-! FUNCTION: Has antimicrobial activity against B.subtilis, E.coli, E.faecalis, P.aeruginosa, and S.aureus. Has insecticidal and hemolytic activities. Probably acts by disturbing membrane function with its amphipathic structure.

-! SUBCELLUIAR LOCATION: Secreted.

-! TISSUE SPECIFICITY: Expressed by the venom gland.

-! ALSSUE SPECIFICITY: Expressed by the venom gland.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20132510; PubMed=10669026; DOI=10.1016/S0041-0101(99)00167-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cupiennin 1, a new family of highly basic antimicrobial peptides in the venom of the spider Cupiennius salei (Ctenidae)."; J. Biol. Chem. 277:11208-11216(2002).
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-!- MASS SPECTROWETRY: MW=3794.89; METHOD=Electrospray; RANGE=1-35; NOTE=Ref.2.
-!- FUNCTION: Antifreeze proteins lower the blood freezing point.
-!- SIMILARITY: Belongs to the type-I AFP family.
PIR, S06417; FDF15G.
Antifreeze protein; Direct protein sequencing; Repeat.
MOD RES 1 Blocked amino end (Met).
SEQÜENCE 33 AA, 2980 MW; 7F2ACC56B70A2080 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -ugranimus satel (manacilla) spuel).
Eukaryota; Metazoa; Arthropas, Chelicerata; Arachnida; Araneae;
Araneomorphae; Entelegynae; Lycosoidea; Ctenidae; Cupiennius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE, SYNTHESIS, FUNCTION, MASS SPECTROMETRY, AND AMIDATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-21909535; PubMed-11792701; DOI=10.1074/jbc.M111099200; Kuhn-Nentwig L., Mueller J., Schaller J., Walz A., Dathe M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amidation; Antibiotic; Direct protein sequencing; Hemolysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22.9%; Score 38; DB 1; Length 35; 50.0%; Pred. No. 3.5e+03; ative 2; Mismatches 8; Indels
                                                                                                                                                                        Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glutamic acid 1-amide.
AE1677338BA73894 CRC64;
                                                                                                                                                                   Query Match 22.9%; Score 38; DB 1; I Best Local Similarity 48.0%; Pred. No. 3.4e+03; Matches 12; Conservative 1; Mismatches 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                 5 AKKEKAAKKAYKKEAKAKAAEAAAK 29
                                                                                                                                                                                                                                                                                                                8 AAKTAADALAAAKKTAADAAAAAK 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cupiennius salei (Wandering spider)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 KKEAKAKAAEAAKEAAYEA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35 AA; 3797 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 22.9°
Best Local Similarity 50.0°
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neurotoxin; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=6928;
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35 AA.

PRT;

PRELIMINARY;

RESULT 15 Q7RC19 ID Q7RC19 AC Q7RC19;

11 KKVAKTVAKQAAKQGAKYVA 30

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Carucci D.J.;
"Genome sequence and comparative analysis of the model rodent malaria gename sequence and comparative analysis of the model rodent malaria parasite Plasmodium yoelii yoelii.";
Parasite Plasmodium yoelii yoelii.";
Paratre 419:512-219(2002).
-i- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                        PubMed=17XNL;
PubMed=1286865; DOI=10.1038/nature01099;
PubMed=1286865; DOI=10.1038/nature01099;
Silva J.C., Emolaeva M.D., Allen J.B., Kooij T.W., Pertea M., Silva J.C., Emolaeva M.D., Allen J.B., Shemmay M.F., Bidwell S.L., Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L., Shallon S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M., Florens L., Yates F.R. III, Raine J.D., Sinden R.B., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., Van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
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0
                                                                                                                                                                                        Plasmodium yoelii yoelii.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 38; DB 2; Length 35;
Pred. No. 3.5e+03;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 35 AA; 4472 MW; D9B2098F0710372A CRC64;
01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     completed: June 3, 2005, 09:59:48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AABLO1001963; EAA18097.1; -. Hypothetical protein.
                                                                                                                 Hypothetical protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 58.3 tes 7; Conservative
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                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Ltď.	
GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.	
GenCore version 5.1.6 c) 1993 - 2005 Compug	model.
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yright	search.
Co	orotein - protein search, using sw model
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Run on:

3, 2005, 09:18:04; Search time 158 Seconds (without alignments) 85.675 Million cell updates/sec

US-10-792-311-1

Title: Perfect score:

1 AKKYAKKEKAAKKAYKKEAKAKAAEAAAKEAAYEA 35 Sequence:

BLOSUM62 Scoring table: 2105692 seqs, 386760381 residues Searched:

Gapop 10.0 , Gapext 0.5

854512 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 35

Post-processing: Minimum Match 1008
Maximum Match 1008
Listing first 45 summaries

A_Geneseq_16Dec04:* .: geneseqp1980s:* ٠. Database

geneseqp2003as:* geneseqp2003bs:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2002s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

SUMMARIES

ion	Copolymer	Peptide 1	Polycatio	Protamine	Peptide m	Polycatio	Protamine	Self-asse	Self-asse	Peptide u	Polycatio	Polycatio	Protamine	Protamine	Flexible	Polycatio	Protamine	Human his	Polycatio	Protamine	Peptide m	Human pol	Peptide 1		
Description	Aay82571	Adn11701	Aar90180	Aaw06686	Aab08168	Aar90181	Aaw06688	Adj81216	Adj81346	Ado43177	Aar90178	Aar90176	Aaw06687	Aaw06697	Abm18907	Aar90179	Aaw06698	Abr42885	Aar90177	Aaw06685	Aab08167	Aa008450	Adn11699	Aaw38224	Aab08175
ID	AAY82571	ADN11701	AAR90180	AAW06686	AAB08168	AAR90181	AAW06688	ADJ81216	ADJ81346	AD043177	AAR90178	AAR90176	AAW06687	AAW06697	ABM18907	AAR90179	AAW06698	ABR42885	AAR90177	AAW06685	AAB08167	AA008450	ADN11699	AAW38224	AAB08175
DB	<u>_</u> ~	æ	7	~	m	~	~	7	7	ω	~	N	~	~	7	~	7	9	7	~	m	4	80	7	m
% Query Match Length	35	31	32	32	32	33	33	25	25	28	29	29	29	29	26	29	29	27	28	28	30	31	26	31	32
% Query Match	100.0	42.8	40.7	40.7	40.7	40.7	40.7	39.2	39.5	38.6	37.7	37.7	37.7	37.7	37.3	36.7	36.7	34.6	34.6	34.6	34.3	33.7	33.1	32.8	32.8
Score	166	71	67.5	67.5	67.5	67.5	67.5	65	65	64	62.5	62.5	62.5	62.5	62	61	61	57.5	57.5	57.5	57	26	55	54.5	54.5
Result No.		7	3	4	S	9	7	80	Q	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

4 AA011831 6 ABP59427 6 ABP59427 6 A AA054715 7 ADJ81345 0 7 ADJ81345 0 7 ADJ81345 0 7 ADJ81345 0 7 ADJ81345 0 6 AAB17118 0 5 AAB17118 1 4 AA011888 1 4 AA011888 1 3 AAB08171 2 AAR8173 3 AAB173 4 3 AAB173 5 AAR8173 6 6 ABR42884 6 2 AAW3573 8 2 AAW38882	Aacil831 Human pol Abp59427 Self-asse Abc959423 Self-asse Abc99423 Self-asse Adj81245 Self-asse Adj81245 Self-asse Adj81245 Self-asse Adj81215 Self-asse Adj81215 Self-asse Adj81215 Self-asse Adol8176 Peptide m Aacil888 Human pol Aabo8171 Peptide m Aacol4674 Human pol Aacol4674 Human pol Abd77360 Selected Abg77360 Selected	
######################################	AAO11831 ABP59423 AAP59423 AAO04715 AAO1415 AAO1115 AAE17118 AAE17118 AAE17110 AAB08170 AAO1674 AAB08171 AAB08178 AAR84173 AAR84173 AAR84173 AAR842884 AAR842884	
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		1

ALIGNMENTS

glatizamer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidabetic; thyromimetic; haemostatic; antipsoriatic; dermatory; antidabetic; thyromimetic; haemostatic; antipsoriatic; dermatory continuament; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; permissis; pemphigus vulgaris; systemic lupus erythematosus. Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:1. Copolymer; molecular weight marker; TV-marker; immune disease; AAY82571 standard; peptide; 35 AA. (first entry) 28-JUL-2000 AAY82571; RESULT 1

Unidentified

VO200018794-A1.

06-APR-2000.

99WO-US022402 24-SEP-1999; 98US-0101693P. 25-SEP-1998; (YEDA) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.

Lis D; 3ad A, WPI; 2000-317499/27.

Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.

Claim 10; Page 14; 72pp; English.

AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides

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cetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune thrombocytopaenia purpura, colitis, contact sease, chronic immune thrombocytopaenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthemia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated mediated diseases which can be treated include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as molecular weight markers
   the invention are used as molecular weight markers for glatiramer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 35 AA;
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Gaps
                                    ö
   Length 35;
                                   Indels
100.0%; Score 166; DB 3;
100.0%; Pred. No. 2.1e-12;
iive 0; Mismatches 0;
                                                                                     1 AKKYAKKEKAAKKAYKKEAKAKAEAAAKEAAYEA 35
                                                                    1 AKKYAKKEKAAKKAYKKEAKAKAAEAAAKEAAYEA 35
 Query Match
Best Local Similarity 100.(
Matches 35; Conservative
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RESULT

ADN11701 standard; protein; 31 AA 15-JUL-2004 (first entry) ADN11701;

Peptide linker SEQ ID NO: 38

enzyme; Cre recombinase; chromosomal translocation; phage; gene inactivation; transgenic; linker.

Synthetic.

EP1413586-A1

28-APR-2004.

21-OCT-2002; 2002EP-00292603.

21-OCT-2002; 2002EP-00292603.

(CNRS) CNRS CENT NAT RECH SCI

Sampieri F; Herman J, Jullien NCG,

WPI; 2004-332811/31. N-PSDB; ADN11700 Use of nucleotide sequence encoding polypeptide sequence comprising fragment of Pl bacteriophage Cre recombinanse, vector containing nucleotide sequence and polypeptide sequence for regulating Pl bacteriophage Cre recombinase activity.

Claim 15; Page 31; 51pp; English.

Novel peptides are claimed which contain 20-40 amino acids and which have a total cationic charge of less than +21 (pref. +16 to +18; esp. +18) as determined by the number of positively charged amino acids in the sequence. Preferably the positive charges are grouped in clusters separated by neutral amino acids. Especially the peptides contain 28-32 amino acids having blocks of 2-4 positively charged amino acids separated by blocks of 2-6 neutral acids. Alternatively the positive charge may be distributed evenly or randomly along the peptide sequence. In particular the peptides are analogues of n-protamine (total cationic charge = +21) in which selected arguine residues have been replaced with uncharged amino acids and other arguine residues have been replaced by other positively charged amino acid residues, preferably lysine. The peptides

reverse the effect of low mol. wt. heparin (LMWH) anticoagulation and hence can be used medically to prevent bleeding after the conclusion of

The present invention relates to the use of a first nucleotide sequence encoding a first polypeptide sequence comprising N-terminal fragment of P1 bacteriophage Cre recombinanse, a second nucleotide sequence encoding a second polypeptide sequence comprising C-terminal fragment of Cre combinase, a vector containing the first and second nucleotide sequences, or first and second polypeptide sequences for regulating activity of P1 bacteriophage Cre recombinase. The sequences are useful for regulating

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1;
       inducing reciprocal chromosomal translocation, for exchanging one DNA cassette for another by recombinase-mediated cassette exchange and for the inactivation of selected genes in transgenic animals. The present sequence is a polypeptide shown in the exemplification of the invention.
                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New poly:cationic polypeptide n-protamine analogues - having reduced cationic charge and lower toxicity, used for reversing (low mol.wt.)
                                                                                                                                                                                                                                                                                                                               n-protamine; anticoagulation reversal; low molecular weight heparin; polycationic; positively charged amino acid; lysine.
activity of the P1 bacteriophage Cre recombinase in cells, for
                                                                                                                     2;
                                                                                              8; Length 31;
                                                                                                                     7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "C-terminal is in amide form"
                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "N-terminal is acetylated"
                                                                                                                                                                                                                                                                                                         Polycationic polypeptide n-protamine analogue.
                                                                                             42.8%; Score 71; DB 8;
64.5%; Pred. No. 0.21;
iive 2; Mismatches
                                                                                                                                             5 AKKEKAAKKAYKKEAKAKAAEAAAKEAAYEA 35
                                                                                                                                                                    1 ASAEAAAKEAAKEAAK--EAAAKEAAKA 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wakefield TW, Stanley JC, Andrews PC;
                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 13; 34pp; English.
                                                                                                                                                                                                                                AAR90180 standard; peptide; 32 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94WO-US012981.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93US-00152488
94US-00303025
                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                        Local Similarity 64.5
les 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              heparin anticoagulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UNMI ) UNIV MICHIGAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1995-193899/25.
                                                                       Sequence 31 AA;
                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9513083-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-SEP-1994;
                                                                                                                                                                                                                                                                                  25-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-MAY-1995.
                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                          AAR90180;
                                                                                               Query Match
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                                                                                                                                                                                                         RESULT 3
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Procualing burging desired from salumning or small broamming to proceed the process of the major components of saluming protein heparin anticogulation. One of the major components of salumine protamine is a 32 amino acid peptide having a total cationic charge of [+21], with argaina accounting for 67% of the total sequence and for all of the positive charge. Peptides of 20-40 amino acids with total cationic charge less than [+21] and which are able, at least partially, to reverse the effect of heparin and/or low modecular weight heparin anticoagulants are claimed. Specifically, the peptides are polycationic analogues of norman where the positive charge on the amino acid sequence is reduced by selective replacement of positively charged arginine residues with an uncharged residue, so that total cationic charge is less than [+21]. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Coagulation, anticoagulant; heparin; platelet aggregation; cell adhesion; positively charged cluster; arginine; polycationic; decrease; n-protamine; salmine protamine; protamine sulphate; salmon sperm.
clinical procedures using heparin therapy. They are less toxic than n-protamine since the reduced positive charge gives an improved efficiency to toxicity ratio; and they may be more effective than n-protamine in their anti-LMWH action. The present sequence (total cationic charge = +18) is a specific example of the new polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3. 30
/label= repeat region
/note= "4 tandem repeats of (Lys)2(Ala)2(Lys)2Ala motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide reversing the anticoagulant effects of heparin - is based on protamine but has fewer positive charges for reduced toxicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protamine sulphate (also called n-protamine or salmine protamine) is
                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                   Score 67.5; DB 2; Length 32;
Pred. No. 0.55;
2; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          1 AKKYAKK-EKAAKKAYKKEAKAKAAEAAKE 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                2 AKKAAKKAAKKAAKKAAKKAAKKAKK 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protamine-like peptide analogue [+18B]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "acetylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 5; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW06686 standard; peptide; 32 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "amidated"
                                                                                                                                                                                                                                                                          40.7%;
61.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96WO-US006567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MICHIGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-011697/01.
                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                            Sequence 32 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wakefield TW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9635444-A1
                                                                                                                                                                                                                                                                                                                                     19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-NOV-1996
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                                                                                                                                                                                                                                                                          Query Match
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LID AAW0

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                                                     y and inexpensive to prepare. The present sequence represents a cific example of a protamine-like peptide with a charge of [+18] which been found to reverse the anticoagulation effects of both standard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a synthetic peptide which has a high affinity for glycoaminoglycans and proteoglycans. The peptide is useful in methods for modulating heparin or other glycoaminoglycans with anticoagulant activity, promoting cell attachment or adhesion to natural or synthetic surfaces (especially vein grafts), modulating tumour cell metastasis, modulating cartilage differentiation, targeting drugs to epithelial cell surfaces (or to other cells expressing proteoglycans), modulating enzymes that act on glycoaminoglycan substrates, affinity purification of bioactive sequences of a glycoaminoglycan, modifying endothelial cell pro-coagulant or anti-coagulant functions mediated through glycoaminoglycans, and modulating wound healing. The peptide may also be used for blocking tissue uptake of heparin or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel synthetic peptides with high affinity for glycoaminoglycans and proteoglycans, useful for modulating heparin, promoting cell attachment, modulating tumor metastasis and modulating wound healing.
peptides are used in vivo to reverse the effects of heparin; they the same anti-heparin activity as protamine but are less toxic sause of the reduced number of positive charges? and are relatively
                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycoaminoglycan; proteoglycan; heparin modulation; anticoagulant; cell attachment; cell adhesion; vein graft; tumour cell metastasis; cartilage differentiation; wound healing.
                                                                                                                                                                                                                       ä
                                                                                                                                                                                   Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide modulating activity of heparin, and other glycans.
                                                                                                                                                                                                                    9; Indels
                                                                                                                                                                                  Score 67.5; DB 2;
Pred. No. 0.55;
                                                                                                                                                                                                                                                         1 AKKYAKK-EKAAKKAYKKEAKAKAAAAKE 30
                                                                                                                                                                                                                                                                                          AKKAAKKAKKAAKKAAKKAKKA 32
                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schick BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 30; 76pp; English
                                                                                                                                                                                                                                                                                                                                                                                      Ź
                                                                                                           and low molecular weight heparin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               San Antonio JD, Verrecchio A,
                                                                                                                                                                                                                                                                                                                                                                                     32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32-FEB-2000; 2000WO-US002853.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0118276P.
                                                                                                                                                                                  Query Match
Best Local Similarity 61.3%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     AAB08168 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-543446/49
                                                                                                                                               Sequence 32 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200045831-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                             34-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
   new peption
                                                      easy and
specific
                                                                                                                                                                                                                                                                                                                                                                                                                         AAB08168;
                                         (because
                                                                                                                                                                                                                                                                                                                                                  RESULT 5
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DB 3; Length 32;

40.7%; Score 67.5;

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Query Match

Pred. No. 0.57;

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a total cationic charge of less than +21 (pref. +16 to +18; esp. +18) as determined by the number of positively charged amino acids in the sequence. Preferably the positively charged amino acids in the sequence. Preferably the positive charges are grouped in clusters separated by neutral amino acids. Especially the peptides contain 28-32 amino acids having blocks of 2-4 positively charged amino acids separated by blocks of 2-6 neutral acids. Alternatively the positive charge may be distributed evenly or randomly along the peptide sequence. In particular the peptides are analogues of n-protamine (total cationic charge = +21) in which selected arginine residues have been replaced by their positively charged amino acid residues, preferably lysine. The peptides reverse the effect of low mol. Wt. heparin (LMWH) anticoagnlation and hence can be used medicially to prevent bleeding after the conclusion of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel peptides are claimed which contain 20-40 amino acids and which have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clinical procedures using heparin therapy. They are less toxic than n-protamine since the reduced positive charge gives an improved efficiency to toxicity ratio; and they may be more effective than n-protamine in their anti-lMWH action. The present sequence (total cationic charge = +16) is a specific example of the new polypeptides
                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New poly:cationic polypeptide n-protamine analogues - having reduced cationic charge and lower toxicity, used for reversing (low mol.wt.)
                                                                                                                                                                                                                                                                                                                           n-protamine; anticoagulation reversal; low molecular weight heparin; polycationic; positively charged amino acid; lysine.
                  3
                  4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "C-terminal is in amide form"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "N-terminal is acetylated"
                                                                                                                                                                                                                                                                                         Polycationic polypeptide n-protamine analogue.
 Pred. No. 0.55;
                  4; Mismatches
                                                                         RKKAAKAARKKAAKAARKKAA 30
                                                    7 KEKAAKKAYKKEAKA---KAAEAAKEAA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Andrews PC;
                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 13; 34pp; English.
                                                                                                                                                                                  AAR90181 standard; peptide; 33 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94WO-US012981.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93US-00152488.
94US-00303025.
 62.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wakefield TW, Stanley JC,
                                                                                                                                                                                                                                                     (first entry)
                18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      heparin anticoagulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UNMI ) UNIV MICHIGAN
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                     Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9513083-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-NOV-1994;
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                                                                                                                                                                                                                                                     25-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                   AAR90181;
                  Matches
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                                                                                                                                              RESULT
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Protamine sulphate (also called n-protamine or salmine protamine) is a polycationic peptide derived from salmon sperm and is used to reverse the parin anticoagulation. One of the major components of salmine protamine is a 32 amino acid peptide having a total cationic charge of [421], with carginine accounting for 67% of the total sequence and for all of the cost into acid peptides of 20-40 amino acids with total cationic charge less than [421] and which are able, at least partially, to reverse the effect of heparin and/or low molecular weight heparin anticoagulants are claimed. Specifically, the peptides are polycationic analogues of nortamine where the positive charge on the amino acid sequence is reduced by selective replacement of positively charged arginine residues with an uncharged residue, so that total cationic charge is less than [+21]. The nortation and provides are used in vivo to reverse the effects of heparin; hey have the same anti-heparin activity as protamine but are less toxic (because of the reduced number of positive charges) and are relatively
                          1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   easy and inexpensive to prepare. The present sequence represents a specific example of a protamine-like peptide with a charge of [+18] which has been found to reverse the anticoagulation effects of both standard and low molecular weight heparin
                                                                                                                                                                                                                                                                                                                                   Coagulation; anticoagulant; heparin; platelet aggregation; cell adhesion; positively charged cluster; arginine; polycationic; decrease; n-protamine; salmine protamine; protamine sulphate; salmon sperm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4. 31
/label= repeat_region
/note= "4 tandem repeats of (Lys)2(Ala)2(Lys)2Ala motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide reversing the anticoagulant effects of heparin - is based on protamine but has fewer positive charges for reduced toxicity.
                          Gaps
                          ï
                          Indels
                          . 6
                                                            1 AKKYAKK-EKAAKKAYKKEAKAKAAEAAKE 30
                                                                                   3 AKKAAKKAKKAAKKAAKKAKKAKKA33
61.3%; Preα. ....
-'''A 2; Mismatches
                                                                                                                                                                                                                                                                                                   Protamine-like peptide analogue [+18BE].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wakefield TW, Stanley JC, Andrews PC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "acetylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 5; 42pp; English.
                                                                                                                                                                                         AAW06688 standard; peptide; 33 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "amidated"
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                                                                                                                                                                                                                                                               (first entry)
                        19; Conservative
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         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-MAY-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                               AAW06688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Region
                          Matches
                                                                                                                                                                            AAW06688
                                                                                                                                                       RESULT
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DB 2; Length 33;

40.7%; Score 67.5;

Sequence 33 AA;

Query Match

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membranes or coatings that absorb specific wavelengths of infrared radiation, and in optical applications e.g., as matrices to align non-linear chromophores which are useful in creating materials for second order non-linear orbits. (II) is useful in hydrogen catalysis, as coatings for blomaterials, saffolds for tissue engineering, ferroelectric materials, artificial muscles, switching devices, etc. This sequence represents a peptide used in the method of the invention.
                                                                                                                                                                            Sequence 25 AA;
          888888888888
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                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a miniblock polymer (I) comprising a self-
fabricating block and a solubilizing block, a block for triggering self-
fabrication by external or environmental conditions, and a block for
incorporating turns in the polymer or for providing sites for chemical
modifications, has a molecular weight of 1000-300000 and, in solution,
can self-fabricate to form 3-dimensional material having long-range
order, and where (I) has glycine content of at least 20%. (I) is useful
for controlled delivery of a drug which involves incorporating adrug
the drug. The drug is incorporated whithin layers of the self-fabricating
material. (II) is useful for modifying the optical response of a device
in the near to mid infrared wavelength range which involves applying (II)
cot forms, which can then undergo very specific structural transitions to
form rigid materials. (I) can be used as structural transitions to
form rigid materials. (I) can be used as structural transitions to
form rigid materials. (I) can be used as structural transitions to
form rigid materials. (I) can be used as structural transitions to
cot forms, which can then undergo very specific structural transitions to
form rigid materials. (I) can be used as structural transitions to
cor forms is useful for preparing chemically patterned templates with either
connolithographic processes. A self-fabricated structure containing the
sensitive devices, IR sensors, IR filters, night telescopes and
thermosensitive detectors. (II) can be used for preparing films,
                                                                       ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Miniblock polymer useful in nanolithographic processes, has self-fabricates fabricating block and solubilizing block, has glycine and self-fabricates to form 3-dimensional materials having long-range orders, in solution.
                                                                                                                                                                                                                                                                                                                                                                                                                         miniblock polymer; optical response; mid infrared wavelength range; long range ordered fluid; liquid crystals; nanolithography; IR-sensitive device; IR sensor; IR filter; inght telescope; thermosensitive detector; non-linear chromophore; blomaterial; tissue engineering scaffold; ferroelectric material; artificial muscle;
                                                                       Gaps
                                                                       1;
                              Length 33;
                                                                       Indels
                                                                       9.
                              DB 2;
                         Score 67.5; DB Pred. No. 0.57; 2; Mismatches
                                                                                                             1 AKKYAKK-EKAAKKAYKKEAKAKAAEAAKE 30
                                                                                                                                     Claim 31; SEQ ID NO 71; 91pp; English
                                                                                                                                                                                                                                                                                                                                                                                    Self-assembling polymer peptide #71
                                                                                                                                                                                                                                                            ADJ81216 standard; peptide; 25 AA
                            40.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-OCT-2001; 2001US-0326743P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-OCT-2002; 2002WO-US031375
                                                                                                                                                                                                                                                                                                                                           06-MAY-2004 (first entry)
                                                                       19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-671392/63.
                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     switching device.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2003056297-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                              Query Match
Best Local 9
                                                                       Matches
                                                                                                                                                                                                                   RESULT 8
ADJ81216
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The invention relates to a miniblock polymer (I) comprising a self-fabricating block and a solubilizing block, a block for triggering self-fabrication by external or environmental conditions, and a block for incorporating turns in the polymer or for providing sites for chemical modifications, has a molecular weight of 1000-300000 and, in solution, can self-fabricate to form 3-dimensional material having long-range order, and where (I) has glycine content of at least 20%. (I) is useful for controlled delivery of a drug which involves incorporating a drug within (I), and administering the self-fabricating material, in is useful for modifying the optical response of a device in the near to mid infrared wavelength range which involves applying (II) to the surface of the device (all claimed). (I) is useful for preparing to the surface of the device (all claimed). (I) is useful for preparing long range ordered fluids (i.e., liquid crystals) in a variety of phases
                                                   ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Miniblock polymer useful in nanolithographic processes, has self-fabricates fabricating block and solubilizing block, has glycine and self-fabricates to form 3-dimensional materials having long-range orders, in solution.
                                                                                                                                                                                                                                                                                                                                                                         miniblock polymer, optical response, mid infrared wavelength range, long range ordered fluid; liquid crystals; nanolithography; IR-sensitive device; IR sensor; IR filter; night telescope; thermosensitive detector; non-linear chromophore; biomaterial; tissue engineering scaffold; ferroelectric material; artificial muscle;
                                                     Gaps
                                                   ..
7
           Score 65; DB 7; Length 25;
Pred. No. 0.84;
                                                   4; Indels
                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 202; 91pp; English.
                                                                                        EKAAKKAYKKEAKAKAAEAAKEAA 32
                                                                                                                          1 EAAAKEAAAKEAAAK--EAAAKEAA 23
                                                                                                                                                                                                                                                                                                                                          Self-assembling polymer peptide #201.
                                                                                                                                                                                                                           Æ
                                                                                                                                                                                                                           ADJ81346 standard; peptide; 25
               39.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-OCT-2002; 2002WO-US031375.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-OCT-2001; 2001US-0326743P. 04-JUN-2002; 2002US-0385809P.
Query Match
Best Local Similarity 72.09
                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kaplan DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TUFT ) TUFTS COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-671392/63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              switching device
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003056297-A2.
                                                                                                                                                                                                                                                                                                    36-MAY-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                ADJ81346;
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form rigid materials. (1) can be used as structural tissue implants, in liquid crystal displays, and for producing high-performance composites. (1) is useful for preparing chemically patterned templates with either general features are specific features. (1) is also useful in nanolithographic processes. A self-fabricated structure containing the polymer (11) is useful for modifying and improving performance of IR-sensors, IR sensors, IR filters, night telescopes and thermosensitive detectors. (II) can be used for preparing films, membranes no coatings that absorb specific wavelengths of infrared radiation, and in optical applications e.g., as matrices to align nonlinear chromophores which are useful in creating materials for second order non-linear orbits. (II) is useful in hydrogen catalysis, as coating for biomaterials, scaffolds for tissue engineering, ferroalectric materials, artificial muscles, switching devices, etc. This sequence represents a peptide used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is that of a peptide of potential use for production of a coded probe useful in the method of the invention. The invention provides methods, apparatus and compositions for the detection, identification and/or sequencing of biomolecules, such as nucleic acids or proteins. Coded probes comprising a probe molecule attached to one or more nano-barcodes are allowed to bind to target molecule(s). After binding and separation from unbound coded probes, the bound coded probes are aligned on a surface and analysed by scanning probe microscopy (SPM). The methods allow the sequencing of long nucleic acid sequences in a single sequencing run, high speed of obtaining sequence data, low cost of
                                                                                                                                                                                                                                                                                                 devices, etc. This
  or forms, which can then undergo very specific structural transitions to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detecting, identifying and sequencing of biomolecules using controlled alignment of nano-barcodes encoding specific information for scanning probe microscopy, useful in the fields of molecular biology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                   5
                                                                                                                                                                                                                                                                                                                                                                                                           DB 7; Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nano-barcode; scanning probe microscopy; probe.
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 39.2%; Score 65; DB 7; Best Local Similarity 72.0%; Pred. No. 0.84; Matches 18; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide used for coded probe synthesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EAAAKEAAAKEAAAK--EAAAKEAA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Page 44; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADO43177 standard; peptide; 28 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-SEP-2003; 2003WO-US029726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-SEP-2002; 2002US-00251152.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Su X, Yamakawa M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                 Sequence 25 AA;
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Novel peptides are claimed which contain 20-40 amino acids and which have a total cationic charge of less than +21 (pref. +16 to +18; esp. +18) as determined by the number of positively charged amino acids in the sequence. Preferably the positive charges are grouped in clusters separated by neutral amino acids. Especially the peptides contain 28-32 amino acids having blocks of 2-4 positively charged amino acids separated by blocks of 2-6 neutral acids. Alternatively the positive charge may be distributed evenly or randomly along the peptide sequence. In particular the peptides are analogues of n-protamine (total cationic charge = +21) in thich selected arguinne residues have been replaced by other positively charged amino acid residues, preferably lysine. The peptides amino acid residues, preferably lysine. The peptides creverse the effect of low mol. Wt. hepatin (LWWH) anticoagulation and hence can be used medically to prevent bleeding after the conclusion of clinical procedures using heparin therapy. They are less toxic than n-protamine since the reduced positive charge gives an improved efficiency
                                                                                                                                           4
sequencing and high efficiency in terms of operator time, and sensitive and accurate detection and/or identification of nucleic acids with low incidence of false positive results.
                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New poly:cationic polypeptide n-protamine analogues - having reduced cationic charge and lower toxicity, used for reversing (low mol.wt.)
                                                                                                                                                                                                                                                                                                                                                                                                                                     n-protamine, anticoagulation reversal; low molecular weight heparin; polycationic; positively charged amino acid; lysine.
                                                                                                                                         5;
                                                                                                       Length 28
                                                                                                                                       7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "C-terminal is in amide form"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "N-terminal is acetylated"
                                                                                                       8;
                                                                                                                                                                                                                                                                                                                                                                                                      Polycationic polypeptide n-protamine analogue.
                                                                                                   DB ...2;
                                                                                                                                       1; Mismatches
                                                                                                                                                                           1 AKKYAKKEKAAKKAYKKEAKAKAAEAAAK 29
                                                                                                                                                                                            2 AKAAAKAAKAAKA--AAAKAAKAAK 28
                                                                                                       Score 64;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wakefield TW, Stanley JC, Andrews PC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                 AAR90178 standard; peptide; 29 AA
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                                                                                                       38.6%;
65.5%;
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                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                         19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                heparin anticoagulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UNMI ) UNIV MICHIGAN.
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                                                                                                       Query Match
Best Local Similarity
                                                                      Sequence 28 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                    25-MAR-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                    AAR90178;
                                                                                                                                         Matches
                                                                                                                                                                                                                                                                 RESULT 11
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Novel peptides are claimed which contain 20-40 amino acids and which have a total cationic charge of less than +21 (pref. +16 to +18; esp. +18) as determined by the number of positively charged amino acids in the sequence. Preferably the positive charges are grouped in clusters sequence. Preferably the positive charges are grouped in clusters are acids having blocks of 2-4 positively the positive charge amino acids separated by blocks of 2-6 neutral acids. Alternatively the positive charge may be distributed evenly or randomly along the peptide sequence. In particular the peptides are analogues of n-protamine (total cationic charge = +21) in which selected arguine residues have been replaced with uncharged amino acids and other arguine residues have been replaced by other positively charged amino acid residues, preferably lysine. The peptides reverse the effect of low mol. Wt. heparin (LMWH) anticoagulation and hence can be used medically to prevent bleeding after the conclusion of clinical procedures using heparin Inbrapy. They are less toxic than n-protamine since the reduced positive charge gives an improved efficiency
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                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New poly:cationic polypeptide n-protamine analogues - having reduced cationic charge and lower toxicity, used for reversing (low mol.wt.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  n-protamine; anticoagulation reversal; low molecular weight heparin; polycationic; positively charged amino acid; lysine.
to toxicity ratio; and they may be more effective than n-protamine i their anti-LMWH action. The present sequence (total cationic charge +16) is a specific example of the new polypeptides
                                                                                                                                             ä
                                                                                                         DB 2; Length 29;
                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "C-terminal can be in amide form"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "N-terminal can be acetylated"
                                                                                                                                             9.
                                                                                                                                                                                                                                                                                                                                                                                                                 Polycationic polypeptide n-protamine analogue.
                                                                                                        Score 62.5; Di
Pred. No. 1.9;
                                                                                                                                           1; Mismatches
                                                                                                                                                                              1 AKKYAKKEKAAKKAYKKEAKAKAAEAAAK 29
                                                                                                                                                                                                 2 AKKAAKKAKKAAKKAKKAAK-KAKKAAKK 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Page 13; 34pp; English.
                                                                                                                                                                                                                                                                                                         AAR90176 standard; peptide; 29 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94WO-US012981.
                                                                                                        37.7%;
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94US-00303025.
                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                        Query Match
Best Local Similarity 62.1
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               heparin anticoagulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UNMI ) UNIV MICHIGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1995-193899/25.
                                                                      Sequence 29 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wakefield TW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                25-MAR-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                            AAR90176;
                                                                                                                                                                                                                                                                      RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                          Coagulation; anticoagulant; heparin; platelet aggregation; cell adhesion; positively charged cluster; arginine; polycationic; decrease; n-protamine; salmine protamine; protamine sulphate; salmon sperm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  claimed. Specifically, the peptides are polycationic analogues of n-
protamine where the positive charge on the amino acid sequence is reduced
by selective replacement of positively charged arginine residues with an
uncharged residue, so that total cationic charge is less than [+21]. The
new peptides are used in vivo to reverse the effects of heparin; they
have the same anti-heparin activity as protamine but are less toxic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2. .29
/label= repeat_region
/note= "4 tandem repeats of Ala(Lys)2(Ala)2(Lys)2 motif"
to toxicity ratio; and they may be more effective than n-protamine in their anti-LMWH action. The present sequence (total cationic charge = +16) is a specific example of the new polypeptides
                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide reversing the anticoagulant effects of heparin - is based on protamine but has fewer positive charges for reduced toxicity.
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                                                                                                                                     9; Indels
                                                                                                      Length
                                                                                                    DB 2;
                                                                                                    Score 62.5; D
Pred. No. 1.9;
                                                                                                                                    1; Mismatches
                                                                                                                                                                     1 AKKYAKKEKAAKKAYKKEAKAKAAEAAAK 29
                                                                                                                                                                                                   2 AKKAAKKAAKKAKKAAK-KAKKAAKK 29
                                                                                                                                                                                                                                                                                                                                                                                            Protamine-like peptide analogue [+16BE].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Andrews PC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "acetylated"
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                                                                                                                                                                                                                                                                                          AAW06687 standard; peptide; 29
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                                                                                                    37.7%;
62.1%;
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                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                    Conservative
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                                                                                                    Query Match
Best Local Similarity
                                                                    Sequence 29 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wakefield TW,
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                                                                                                                                    18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
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                                                                                                                                     Matches
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                easy and inexpensive to prepare. The present sequence represents a specific example of a proteamine-like peptide with a charge of [+16] which has been found to reverse the anticoagulation effects of both standard and low molecular weight heparin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coagulation, anticoagulant; heparin; platelet aggregation; cell adhesion; positively charged cluster; arginine; polycationic; decrease; n-protamine; salmine protamine; protamine sulphate; salmon sperm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2...29
/label= repeat region
/note= "4 tandem repeats of Ala(Lys)2(Ala)2(Lys)2 motif"
positive charges) and are relatively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protamine sulphate (also called n-protamine or salmine protamine) is a
                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
                                                                                                                                                                                                                                                                                                                                                                                                                                   Protamine-like peptide analogue P(AK2A2K2)4 with a charge of [+16].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide reversing the anticoagulant effects of heparin - is based protamine but has fewer positive charges for reduced toxicity.
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                                                                                                                                        DB 2; Length 29;
                                                                                                                                                                        9; Indels
                                                                                                                                                        1.9;
                                                                                                                                                                        1; Mismatches
                                                                                                                                      Score 62.5;
Pred. No. 1.8
                                                                                                                                                                                                          1 AKKYAKKEKAAKKAYKKEAKAKAAEAAAK 29
                                                                                                                                                                                                                              Stanley JC, Andrews PC;
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 of the reduced number of
                                                                                                                                                                                                                                                                                                                                AAW06697 standard; peptide; 29 AA.
                                                                                                                                      37.7%;
62.1%;
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                                                                                                      Sequence 29 AA;
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                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a novel isolated polypeptide of Streptococcus pneumoniae. A polypeptide of the invention has antibacterial, antiinflammatory, and auditory activity, and is used as a vaccine. The polypeptide or pharmaceutical composition is useful for the prophylactic or therapeutic treatment of streptococcal infection, meningitis, otitis media, bacteraemia or pneumonia infection. The kit is useful for detecting or diagnosing streptococcal infection. The pharmaceutical composition is useful as vaccine. The polymucleotides are useful in designing DNA probes for detecting circulating Streptococcus in a biological sample. The present sequence is used in the exemplification of the invention. Note: The sequence data for this patent is not fully information supplied by the European Patent Office
              have the same anti-heparin activity as protamine but are less toxic (because of the reduced number of positive charges) and are relatively easy and inexpensive to prepare. The present sequence represents a specific example of a protamine-like peptide with a charge of [+16] which has been found to reverse the anticoagulation effects of both standard and low molecular weight heparin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polypeptides of Streptococcus pneumoniae, useful for diagnosing, preventing or treating streptococcal infection, meningitis, otitis media, bacteremia or pneumonia infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibacterial; antiinflammatory; auditory; vaccine; meningitis; streptococcal infection; otitis media; bacteraemia; pneumonia; linker.
                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouellet C;
                                                                                                                                                                                                             1;
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                                                                                                                                                                                                           9; Indels
                                                                                                                                                                          2; Length
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                                                                                                                                                                          DB
                                                                                                                                                                       Score 62.5; DB; Pred. No. 1.9; 1; Mismatches
                                                                                                                                                                                                                                              1 AKKYAKKEKAAKKAYKKEAKAKAAEAAK 29
                                                                                                                                                                                                                                                                 2 AKKAAKKAKKAAKKAAK-KAKKAAKK 29
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Labbe S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 9; Page 51; 79pp; English
                                                                                                                                                                                                                                                                                                                                                                        ABM18907 standard; peptide; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-DEC-2001; 2001US-0341252P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-DEC-2002; 2002WO-CA002006.
                                                                                                                                                                          37.7%;
62.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Flexible linker peptide L1
                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                             18; Conservative
                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                         Sequence 29 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                            13-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
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2; Gaps 1; 4; Indels Matches 17; Conservative 2; Mismatches

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Search completed: June 3, 2005, 09:56:50 Job time: 160 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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87,672 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_MEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/PCT_MEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
7/cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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11: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US10B_PUB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US10B_PUB.pubpaB_PUB.pubpaa/US10B_PUB.pubpaa/US10B_PUB.pubpaa/US10B_PUB.pubpaa/U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             373443
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AKKYAKKEKAAKKAYKKEAKAKAAEAAKEAAYEA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1465611 seqs, 345679903 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                             OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
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166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
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	Appli	, Appli	1, Appl	1, Appl	119, App	, Appli	69, Appl	3, Appl	0, Appl	8, Appl	41097,	60178,	128, App
Description	Sequence 1, Appli	Sequence 1, Appli	Sequence 71,	Sequence 2	Sequence 1	Sequence 7	Sequence 6	Sequence 7	Sequence 7	Sequence 68, Appl	Sequence 2	Sequence 1	Sequence 1
ĪD	US-09-816-989A-1	US-10-792-311-1	US-10-490-799-71	US-10-667-004-21	US-10-324-143-119	US-09-988-165B-7	US-10-192-832-69	US-10-192-832-73	US-10-490-799-70	US-10-192-832-68	US-10-424-599-241097	US-10-437-963-160178	US-10-909-119-128
DB	σ	17	17	16	15	10	14	14	17	14	15	16	11
% Query Match Length DB	35	35	25	28	26	27	30	30	20	30	35	34	21
Query Match	100.0	100.0	39.2	38.6	37.3	34.6	31.9	31.9	31.3	31.3	31.3	30.7	30.1
Score	166	166	65	64	62	57.5	53	53	52	52	52	51	20
Result No.	1	7	m	4	2	9	7	80	σ,	10	11	12	13

Sequence 6, Appli Sequence 22, Appl	23,	24.	6 2,	25,	Sequence 26, Appl	Sequence 27, Appl	121,	28,	Sequence 122, App	29, 4	Sequence 123, App	Sequence 198091,	Sequence 60, Appl	Sequence 61, Appl	Sequence 2, Appli	6	Seguence 163624,	Sequence 63, Appl	Sequence 119, App	e 26,	Seguence 15, Appl	Seguence 64, Appl	Sequence 120, App		Sequence 66, Appl	67,	Ö	Sequence 272273,	Sequence 4, Appli	24,
10 US-09-988-165B-6 9 US-09-805-301-22	9 US-09-805-301-23	9 US-09-805-301-24	15 US-10-308-322-2	9 US-09-805-301-25	9 US-09-805-301-26	9 US-09-805-301-27	9 US-09-805-301-121	9 US-09-805-301-28	9 US-09-805-301-122	9 US-09-805-301-29	9 US-09-805-301-123	15 US-10-424-599-198091	9 US-09-805-301-60	9 US-09-805-301-61	9 US-09-124-280A-2	9 US-09-805-301-62	15 US-10-424-599-163624	9 US-09-805-301-63	9 US-09-805-301-119	15 US-10-296-879-26	16 US-10-471-895-15	9 US-09-805-301-64	9 US-09-805-301-120	9 US-09-805-301-65	9 US-09-805-301-66	9 US-09-805-301-67	15 US-10-424-599-236809	15 US-10-424-599-272273	15 US-10-333-313-4	US-1
25	53	30	30	31	32	33	33	34	34	35	35	35	28	59	30	30	30	31	31	31	31	32	32	33	34	32	32	32	35	28
		50 30.1		50 30.1		50 30.1	m	50 30.1	50 30.1	e		50 30.1	49 29.5	49 29.5	49 29.5	49 29.5	~	49 29.5	49 29.5	49 29.5	49 29.5	49 29.5	49 29.5	~	49 29.5	49 29.5	49 29.5	49 29.5	49 29.5	48.5 29.2
14 15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Sequence 1, Application US/0981698A

Sequence 1, Application US/0981698A

Sequence 1, Application US/0981698A

Sequence 1, Application US/0981698A

GENERAL INFORMATION:
APPLICANT: Gad, Alexander

APPLICANT: Gad, Alexander

TITLE OF INVENTION: COPCLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKS

TITLE OF INVENTION: AND FOR THERAPEUTIC USE

FILE REFERENCE: 2609/60807-A-PCT-US

CURRENT APPLICATION NUMBER: US/09/816,989A

CURRENT PELING DATE: 2001-03.23

PRIOR PILING DATE: 1998-09-25

PRIOR PILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 7

SEQ ID NO 1

SEQ ID NO 1

LENGTH: 35

LENGTH: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AKKYAKKEKAAKKAYKKEAKAKAAEAAAKEAAYEA 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Matches
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RESULT 2

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APPLICANT: TWTEL CORPORATION
APPLICANT: TWTEL CORPORATION
APPLICANT: GHAN, Selena
APPLICANT: TYMAKAWA, Mineo
APPLICANT: YAMAKAWA, Mineo
TITLE OF INVENTION: SCANNING PROBE MICROSCOPY (SPM)
TITLE OF INVENTION: SCANNING PROBE MICROSCOPY (SPM)
CURRENT APPLICATION NUMBER: US/10/667,004
CURRENT APPLICATION NUMBER: US/10/677,004
CURRENT PILING DATE: 2003-09-19
PRIOR FILING DATE: 2002-09-20
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3:1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Indels
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APPLICANT: CHARLAND, NATHALIE
APPLICANT: BRODEN, BERNARD R.
APPLICANT: MARTIN, DENIS
APPLICANT: MARTIN, DENIS
APPLICANT: BLAIS, NORMAND
APPLICANT: BULBIS, NORMAND
APPLICANT: BULBIS, NORMAND
APPLICANT: BULBIS, NORMAND
TITLE OF INVENTION: STREPTOCOCCUS ANTIGENS
FILE REFERENCE: 55190-56
CURRENT APPLICATION NUMBER: US/10/324,143
CURRENT APPLICATION NUMBER: 60/341,252
PRIOR APPLICATION NUMBER: 60/341,252
PRIOR FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PATENTIN VEY: 2.1
SEQ ID NO 119
LENGTH: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AKKYAKKEKAAKKAYKKEAKAKAAEAAAK 29
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Pred. No. 1
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; OTHER INFORMATION: Synthetic peptide
US-10-667-004-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 119, Application US/10324143
Publication No. US20030232976A1
GENERAL INFORMATION:
                                                            Sequence 21, Application US/10667004
Publication No. US20040126820A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 38.6%;
Best Local Similarity 65.5%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 68.0 Matches 17; Conservative
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                                                                             ## APPLICANT: Gad, Alexander

## APPLICANT: Gad, Alexander

## APPLICANT: Gad, Alexander

## APPLICANT: Gad, Alexander

## APPLICANT: Lis, Doris

## TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK

## TITLE OF INVENTION: AND FOR THERAPEUTIC USE

## FILE REFERENCE: 2609/60807-A-PCT-US

## CURRENT APPLICATION NUMBER: US/09/816,989

## RIOR PILING DATE: 2004-03-02

## PRIOR FILING DATE: 1998-09-25

## RIOR APPLICATION NUMBER: PCT/US99/22402

## RIOR APPLICATION NUMBER: PCT/US99/22402
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; Sequence 7.4, Application US/200500641A1
; GENERAL INFORMATION:
; APPLICANT: VALUGZI, REGINA
; APPLICANT: RALDIZI, REGINA
; TITLE OF INVENTION: THEREFROM
; TITLE OF INVENTION: THO 29.01
; CURRENT APPLICATION NUMBER: US/10/490,799
; CURRENT APPLICATION NUMBER: GO/326,743
; PRIOR FILLING DATE: 2002-10-02
; PRIOR FILLING DATE: 2002-10-02
; PRIOR FILLING DATE: 2002-06-04
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PALENTH VET. 2.1
; SEQ ID NO 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-10-792-311-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 166; DB 17; Best Local Similarity 100.0%; Pred. No. 1.7e-11; Matches 35; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AKKYAKKEKAAKKAYKKEAKAKAAEAAKEAAYEA 35
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Sequence 1, Application US/10792311
Publication No. US20050038233A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 18; Conserv
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US-10-192-832-68
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US-10-192-832-73
                                                                                                                                                                     FEATURE:
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      Sequence 7, Application US/09988165B
Publication No. US20030144473A1
GENERAL INFORMATION:
APPLICANT: Symbiotec Gesellschaft zur Erforschung und Entwicklung
APPLICANT: auf dem Gebiet der Biotechnologie mbH
TITLE OF INVENTION: Peptides for the Production of Preparations
TITLE OF INVENTION: for the Diagnosis and Therapy of Autoimmune Diseases
FILE REFERENCE: 3642
CURRENT APPLICATION NUMBER: US/09/988,165B
CURRENT FILING DATE: 2001-11-19
PRIOR FILING DATE: 1992-09-16
NUMBER OF SEQ ID NOS: 31
SEQ ID NO S: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-192-832-69
Sequence 69, Application US/10192832
Publication No. US20030176335A1
Publication No. US20030176335A1
GENERAL INFORMATION:
APPLICANT: ZHANG, SHUGUANG
APPLICANT: VAUTHEY, SYLVAIN
ITILE REFERENCE: MTV-043.01
CURRENT PAPLICATION NUMBER: US/10/192,832
CURRENT FILING DATE: 2002-07-10
PRIOR FILING DATE: 2001-07-10
PRIOR FILING DATE: 2001-07-10
NUMBER OF SEQ ID NOS: 76
SOFTWARE: PATCHTIN VOIL OF 10
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APPLICANT: ZHANG, SHUGUANG
APPLICANT: VAUTHEY, SYLVAIN
ITILE OF INVENTION: SURFACTANT PEPTIDE NANOSTRUCTURES, AND USES THEREOF
FILE REFERENCE: MTV-043.01
CURRENT APPLICATION NUMBER: US/10/192,832
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US-10-192-832-69
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33;
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Pred. No. 9.4;
2; Mismatches 8;
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Publication No. US20030176335A1
GENERAL INFORMATION:
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56.7%;
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ORGANISM: Artificial Sequence
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Best Local Similarity
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ORGANISM: human
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IS-09-988-165B-7
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LENGTH: 30
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APPLICANT: VALLUZZI, REGINA
APPLICANT: VALLUZZI, REGINA
TITLE OF INVENTION: SLIP-ASSEMBLING POLYMERS, AND MATERIALS FABRICATED
TITLE OF INVENTION: THEREFROM
FILE REFERENCE: TUV-029.01
CURRENT APPLICATION NUMBER: US/10/490,799
CURRENT FILING DATE: 2004-03-25
PRIOR APPLICATION NUMBER: PCT/US02/31375
PRIOR APPLICATION NUMBER: 60/326,743
PRIOR APPLICATION NUMBER: 60/326,743
PRIOR PILING DATE: 2001-10-02
PRIOR PILING DATE: 2002-06-04
NUMBER OF SEQ ID NOS: 163
SOFTWARE: PATENTIN VOY: 2.1
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APPLICANT: ZHANG, SHUGUANG
TITLE OF INVENTION: SURRACTANT PEPTIDE NANOSTRUCTURES, AND USES THEREOF
FILE REPERENCE: MTV-043.01
CURRENT APPLICATION NUMBER: US/10/192,832
CURRENT FILING DATE: 2002-10
PRIOR APPLICATION NUMBER: 60/304,256
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US-10-490-799-70
                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide
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31.3%; Score 52; DB 17; Length 20;
Best Local Similarity 68.2%; Pred. No. 28;
Matches 15; Conservative 1; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                    Score 53; DB 14;
Pred. No. 33;
2; Mismatches 10,
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CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION UNMBR: 60/304,256
PRIOR FILING DATE: 2001-07-10
NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 73
LERGTH: 30
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Publication No. US20030176335A1
GENERAL INFORMATION:
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Sequence 70, Application US/10490799; Publication No. US20050090641A1; GENERAL INFORMATION:
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                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                           14; Conservative
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Gaps

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TITLE OF INVENTION: Human Skin Equivalents Expressing Exogenous Polypeptides FILE REPERENCE: STRAFA-09123 CURRENT APPLICATION NUMBER: US/10/909,119 CURRENT PILING DATE: 2004-07-30 NUMBER OF SEQ ID NOS: 128 SOFTHARE: Patentin version 3.2 SEQ ID NO 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Symbiotec Gesellschaft zur Erforschung und Entwicklung APPLICANT: Symbiotec Gesellschaft zur Erforschung und Entwicklung APPLICANT: auf dem Gebiet der Biotechnologie mbH TITLE OF INVENTION: Peptides for the Production of Preparations TITLE OF INVENTION: for the Diagnosis and Therapy of Autoimmune Diseases FILE REFERENCE: 3642
CURRENT APPLICATION NUMBER: US/09/988,165B
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: US Serial Number 07/946,180
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                                                                                                                                                                                                                                             16; Length 34
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                                                                                                                                           OTHER INFORMATION: Clone ID: PAT_MRT4530_59481C.1.pep
                                                                                                                                                                                                                                          30.7%; Score 51; DB 57.1%; Pred. No. 62; tive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
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Sequence 128, Application US/10909119; Publication No. US20050079578A1
EDEREAL INFORMATION:
APPLICANT: Centanni, John M.
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54.2%;
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Best Local Similarity 65.2%
                                                                                                                                                                                                                                                                             Best Local Similarity 57.1
Matches 12; Conservative
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SEQ ID NO 6
                                         TYPE: PRT
ORGANISM: Oryza sativa
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Best Local Similarity
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ORGANISM: human
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          LENGTH: 34
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                                                                                                            FEATURE:
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APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Bunkharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
AP
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APPLICANT: La Rovalic David K
APPLICANT: Eavour Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENT APPLICATION NUMBER: 105/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 241097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 31.3%; Score 52; DB 14; Length 30; Best Local Similarity 59.1%; Pred. No. 42; Matches 13; Conservative 2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31.3%; Score 52; DB 15; Length 35; 60.0%; Pred. No. 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: PAT_MRT3847_59739C.1.pep
US-10-424-599-241097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 241097, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 160178, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 KAAKKAYKKEAKAKAAEAAKE 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KKKKKKKKKKAAAAAAAKK 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 KKKKKKEKNKKKSYIKKYKA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 KKYAKKEKAAKKAYKKEAKA 21
                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
PRIOR FILING DATE: 2001-07-10
NUMBER OF SEQ ID NOS: 76
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 68
LENGTH: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 60.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-437-963-160178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-424-599-241097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 160178
                                                                                                                                                                                                                                                                                                                                            US-10-192-832-68
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us-10-792-311-1.rapb

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30.1%; Score 50; DB 9; Length 28;
Best Local Similarity 42.9%; Pred. No. 65;
Matches 12; Conservative 3; Mismatches 13; Indels
  9; Indels
                                                                                                                                                                                                                                                APPLICANT: Smith, Louis C.
Sparrow, James T.
Hauer, Jochen
Mims, Martha P.
TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 6.0
SOFTWARE: Word Perfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/805,301
FILING DATE: 12-Mar-2001
CLASSIFICATION NUMBER: 08/584,043
APPLICATION NUMBER: 08/584,043
FILING DATE: cUnknown>
APPLICATION NUMBER: 08/584,043
FILING DATE: cUnknown>
APPLICATION NUMBER: 21,7189
FILING DATE: cUnknown>
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 21,7189
TELEFAM: (213) 955-0440
TELEFAM: (213) 955-0440
TELEFAM: (213) 955-0440
TELEFAM: 28 amino acids
INFORMATION CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-805-301-22
                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 470
                                         7 KEKAAKKAYKKEAKAKAAEAAKE 30
                                                                 Sequence 22, Application US/09805301; Patent No. US20020173456A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Los Angeles
STATE: California
13; Conservative
                                                                                                                                            RESULT 15
US-09-805-301-22
Matches
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Gaps

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2 KKYAKKEKAAKKAYKKEAKAKAAEAAAK 29 T KKKKKKKKKKKKKKKKTK 28

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Search completed: June 3, 2005, 10:11:47 Job time: 139 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

June Run on:

3, 2005, 09:48:15 ; Search time 41 Seconds (without alignments) 63.725 Million cell updates/sec

US-10-792-311-1

166 Title: Perfect score: Seguence:

1 AKKYAKKEKAAKKAYKKEAKAKAAEAAKEAAYEA 35

Gapop 10.0 , Gapext 0.5

BLOSUM62

Scoring table:

513545 seqs, 74649064 residues Searched:

250370 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 35

Post-processing: Minimum Match 08 Maximum Match 100

Maximum Match 100% Listing first 45 summaries

Database

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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query	Length	80	ΩI	Description
1	166	100.0	35	4	US-09-405-743A-1	Sequence 1, Appli
7	166	100.0	35	4	US-09-816-989A-1	ť
٣	67.5	40.7	32	Н	US-08-152-488-13	ä
4	67.5	40.7	32	-	US-08-303-025-15	Sequence 15, Appl
Ŋ	67.5	40.7	32	П	US-08-677-304-13	Ë
9	67.5	40.7	32	~	US-08-436-703B-2	'n
7	67.5	40.7	33	٦	8	16,
80	67.5	40.7	33	~	US-08-436-703B-4	4
6	62.5	37.7	29	ч	US-08-152-488-10	Н
10	62.5	37.7	29	-	US-08-152-488-11	11,
11	62.5	37.7	29	-	US-08-303-025-10	10,
12	62.5	37.7	29	-	-08-	11,
13	62.5	37.7	29	Н	US-08-303-025-13	13,
14	62.5	37.7	29	-	US-08-677-304-10	10,
15	62.5	37.7	29	-	US-08-677-304-11	11,
16	62.5	37.7	29	~	US-08-436-703B-3	'n
17	62.5	37.7	29	~	US-08-436-703B-15	15,
18	61	36.7	29	-	US-08-152-488-12	Sequence 12, Appl
19	61	36.7		-	US-08-303-025-14	14,
20	61	36.7		-	0	12,
21	61	36.7		~	-436	16,
22	57.5	34.6		-	US-08-303-025-12	12,
23	57.5	34.6		~	US-08-436-703B-1	1, 1
24	54.5	32.8		4	US-09-221-050-2	~
25	50	ö		~	US-08-894-339-6	9
56	20	30.1	26	m	-60-	9
27	20	30.1	28	٣	US-08-584-043A-22	22,

Sequence 23, Appl Sequence 24, Appl Sequence 25, Appl	Sequence 26, Appl		Sequence 122, App Sequence 29, Appl	123,	28,	4, A	28, 7	Sequence 28, Appl
US-08-584-043A-23 US-08-584-043A-24 US-08-584-043A-25	US-08-584-043A-26	US-08-584-043A-121 US-08-584-043A-121 US-08-584-043A-28	US-08-584-043A-122 US-08-584-043A-29	US-08-584-043A-123 US-08-995-172-2	US-08-839-624-28 US-09-150-812-28	US-09-247-054-4 US-08-231-730A-28	US-08-427-001C-28	US-08-457-171-28
29 30 31 30	32 2	3 3 3 5 4 3 3 5 3 4 5 6 6 7 7 6 7 7 7 7 7	34 35 3	35 3	31 3	31 4 32 1	32 1	32 1
50 30.1 50 30.1 50 30.1		50 30.1			49.5 29.8 49.5 29.8	49.5 29.8 49.5 29.8	0, 0	49.5 29.8
7 5 8 7 6 8	31	1 E E	35 36	37	33 6 4 0 0	41	43	. 4 .

ALIGNMENTS

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SYNTHETIC
Sequence 1, Application US/09405743A
; Sequence 1, Application US/09405743A
; Patent No. 6514938
; Patent No. 6514938
; GENERAL INFORMATION:
    APPLICANT: Yeda Research and Development Co., Ltd.
    TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
    FILE REFERENCE: 60807-A
    FULE REFERENCE: 69807-A
    NUMBER OF SEQ ID NOS: 7
    SOFTWARE: PatentIn Ver. 2.1
    SEQ ID NO 1
    LENGTH: 35
                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
, THER INFORMATION: Description of Artificial Sequence:
, OTHER INFORMATION: PEPTIDE
US-09-405-743A-1
                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
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Gaps ö Query Match 100.0%; Score 166; DB 4; Length 35; Best Local Similarity 100.0%; Pred. No. 3e-13; Matches 35; Conservative 0; Mismatches 0; Indels

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1 AKKYAKKEKAAKKAYKKEAKAKAAEAAKEAAYEA 35 1 AKKYAKKEKAAKKAYKKEAKAKAAEAAAKEAAYEA 35

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APPLICANT: dad, Alexander
APPLICANT: dad, Alexander
APPLICANT: dad, Alexander
APPLICANT: dad, Doxis
APPLICANT: dis, Doxis
APPLICANT: dis, Doxis
APPLICANT: dis, Doxis
APPLICANT: dis, Doxis
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
FILE REPERENCE: 2609/60807-A-PCT-US
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR PILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR APPLICATION NUMBER: PCT/US99/22402 Sequence 1, Application US/09816989A Patent No. 6800287 GENERAL INFORMATION: RESULT 2 US-09-816-989A-1 g

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1 AKKYAKK-EKAAKKAYKKEAKAKAAEAAKE 30
                                                  2 AKKAAKKAKKAAKKAAKKAKKAKKA 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                       US-08-303-025-15
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATUME:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-1
                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 40.7%; Score 67.5; DB 1; Length 32; 1 Similarity 61.3%; Pred. No. 0.1; 19; Conservative 2; Mismatches 9; Indels
                                                                                                                                    DB 4; Length 35,
                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                              ; Sequence 13, Application US/08152488
; Faquence 13, Application US/08152488
; Fatent No. 5544619
; GENERAL INFORMATION:
; APPLICANT: Wakefield, Thomas W.
; APPLICANT: Stanley, James C.
; TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN TITLE OF INVENTION: ANTICOAGULATION REVERSAL
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
                                                                                                                                Query Match 100.0%; Score 166; DB 4; Best Local Similarity 100.0%; Pred. No. 3e-13; Matches 35; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                         1 AKKYAKKEKAAKKAYKKEAKAKAAEAAKEAAYEA 35
                                                                                                                                                                                                                                                1 AKKYAKKEKAAKKAYKKEAKAKAEAABAKEAAYEA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COKRESPONDENCE ADDRESS:
COKRESPONDENCE ADDRESS:
CITY: Cranford
STATE: New Jersey
COUNTRY: United States of America
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07016-1811
COMPUTER READDBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATION G SYSTEM: MS-DOS
SOFTWARE: WORDERfect 6; ASCII (DOS) Text
APPLICATION NAMBER: US/08/152,488
FILING DATE: 12-NOV-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
ATTORNEY AGENT INFORMATION:
ANDAREY AGENT INFORMATION:
ANDAREY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Rohm, Benita J.
REGISTRATION NUMBER: 28,664
REFERENCE/DOCKET NUMBER: RM-7WG
TELECOMUNICATION INFORMATION:
TELEPHONE: 908-276-3344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS: LENGTH: 32 amino acids TYPE: amino acid STRANDEDNES: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: N/A PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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Gaps

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Matches

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Gaps
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40.7%; Score 67.5; DB 1; Length 32;
Best Local Similarity 61.3%; Pred. No. 0.1;
Matches 19; Conservative 2; Mismatches 9; Indels
                                                GENERAL INFORMATION:
APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley C.
TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN TITLE OF INVENTION: ANTICOAGULATION REVERSAL NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benita J, Rohm, Esq.
                                                                                                                                                                                                                                                                                                                                                                                                                                    CALF: 48.25.44.12.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy diskette 3.5" 1.44Mb
COMPUTER: IBM FOC Compatible
OPERATING SYSTEM: MS-DOS V.6.22
SOFTWARE: WordPerfect 6.1; ASCII (DOS) Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,025
FILING DATE: 08-SEPT-1994
CLASSIPICATION BATA:
APPLICATION NUMBER: PCT/US92/06829
FILING DATE: 14-AUG-1992
APPLICATION NUMBER: DCT/US92/06829
FILING DATE: 11-AUG-1992
APPLICATION NUMBER: US 08/152,488
FILING DATE: 12-NOV-1993
ATTORNEY/AGRIT INFORMATION:
NAME: ROAM, BENICA J.
REFERENCE/DOCKET NUMBER: 7WH-060548-00231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 AKKAAKKAKKAKKAAKKAKKAAKKAKK 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AKKYAKK-EKAAKKAYKKEAKAKAAEAAKE 30
                                                                                                                                                                                                                                                                    ADDRESSEE: Benita J. Rohm, Bsg.
STREET: 150 West Jefferson, Suite 2500
CITY: Detroit
                                                                                                                                                                                                                                                                                                                                                                STATE: Michigan
COUNTRY: United States of America
ZIP: 48226-4415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOCUMENT NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
Sequence 15, Application US/08303025
Patent No. 5614494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 13, Application US/08677304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         313-496-7622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 313-496-8454
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE: N/A DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
US-08-677-304-13
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Query Match
40.7%; Score 67.5; DB 2; Length 32;
Best Local Similarity 61.3%; Pred. No. 0.1;
Matches 19; Conservative 2; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 16, Application US/08303025
Fatent No. 5614494
GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND TITLE OF INVENTION: NOW MOLECULAR WEIGHT HEPARIN TITLE OF INVENTION: ANTICOAGULATION REVERSAL
NUMBER OF SEQUENCES: 16
CORRESPONDENCE:
CORRESPONDENCE:
ADDRESSEE: Benita J, Rohm, Esq.
STREET: 150 West Jefferson, Suite 2500
TITLE OF INVENTION: WEIGHT HEPARIN
TITLE OF INVENTION: ANTICOAGULATION REVERSAL
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benita J, Rohm, Esq.
STREET: 6601 Woodward Avenue
STREET: Suite 1525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7WK-060548-00233
                                                                                                                                                                                                                                  COUNTRY: United CLOUDER
ZIP: 48226
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk 1.44Mb, 3.5"
COMPUTER: IBM PC comparible
OPERATING SYSTEM: MS-DOS
SOFTWARE: MORDERFECT 6;
SOFTWARE: ASCII (DOS) Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,703B
FILING DATE: 08-MAY-1995
CLASSIFICATION NUMBER: N/A
PRICE APPLICATION NUMBER: N/A
PRICE APPLICATION NUMBER: N/A
ATTORNEY/AGENT INFORMATION:
NAME: ROHM, Benita J.
REGISTRATION NUMBER: 28,664
REFERENCE/DOCKET NUMBER: 7WK-060548-00;
TELEPHONE: 313-965-1976
TELEPHONE: 313-965-1976
TELEPHONE: 313-965-1976
TELEPHONE: SEQUENCE THANDER: SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AKKYAKK-EKAAKKAYKKEAKAKAAEAAKE 30
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RY: United States of America
48226-4415
                                                                                                                                                                            CITY: Detroit
STATE: Michigan
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTE: MALLO ALLO
TOPOLOGY: N/A
TOPOLOGY: N/A
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: N/A
PUBLICATION INFORMATION:
TITLE: N/A
US-08-436-703B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Detroit
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COUNTRY:
ZIP: 4822
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                                              APPLICANT: Makefield, Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN TITLE OF INVENTION: ANTICOAGULATION REVERSAL NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benita J, Rohm, Esq.
STREET: 512 Springfield Avenue
CITY: Cranford
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                            COUNTRY: United States of America
ZIP: 07016-1811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTMARE: WordPerfect 6; ASCII (DOS)Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/677,304
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Patent No. 5919761
GENERAL INFORMATION:
APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: NOVEL PEPTIDES FOR
TITLE OF INVENTION: HEPARIN AND LOW MOLECULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AKKYAKK-EKAAKKAYKKEAKAKAAEAAKE 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 530
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/152,488
FILING DATE: 12-NOV-1993
APPLICATION NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
ATORNEY/AGENT INPORMATION:
NAME: ROAM, Benite J.
REGISTRATION NUMBER: 26,664
FELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECHOUS: 908-276-3344
INPORMATION: OB-276-5543
INPORMATION: SEQUENCE CHARACTER.FSTICS:
LENGTH: 32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: No. 5721212 Relevant
TOPOLOGY: No. 5721212 Relevant
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORIGINAL SOURCE:
PUBLICATION INFORMATION:
AUTHORS: N/A
                                                                                                                                                                                                                                                                                                                     New Jersey
(: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PUBLICATION INFORMATION:
DOCUMENT NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
                            GENERAL INFORMATION:
  Patent No. 5721212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-436-703B-2
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40.7%; Score 67.5; DB 2; Length 33; 61.3%; Pred. No. 0.11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10, Application US/08152488

Sequence 10, Application US/08152488

Batent No. 5534619

GENERAL INFORMATION:

APPLICANT: Wakefield, Thomas W.

APPLICANT: Stanley, James C.

TITLE OF INVENTION: NOWEL PEPTIDES FOR HEPARIN AND TITLE OF INVENTION: NOWELECTIAR WEIGHT HEPARIN TITLE OF INVENTION: ANTICOAGULATION REVERSAL NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Benita J, Rohm, Esq.

STREET: 512 Springfield Avenue

CITY: Cranford

STATE: Wew Jersey

COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6; ASCII (DOS) Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/152,488
FILING DATE: 12-NOV 1993
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
ATTORNEY, AGENT INFORMATION:
NAME: ROAM: Benita J.
NAME: ROAM: Benita J.
REGISTRATION NUMBER: 28,664
                                                                                                                                                                                                                        7WK-060548-00233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AKKYAKK-EKAAKKAYKKEAKAKAAEAAKE 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
UMBER: US/08/436,703B
08-MAY-1995
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-276-3344
                        FILING DATE: 08-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION 514
APPLICATION NUMBER: N/A
FILING DATE: N/A
ATTORNEY/AGENT INFORMATION:
NAME: ROHM, Benita J.
REGISTRATION NUMBER: 28,664
REFERENCE/DOCKET NUMBER: 7WK-1
TELECOMMUNICATION INFORMATION:
TELECHONE: 313-965-1976
TELEFPAX: 313-965-1976
                                                                                                                                                                                                                                                                    TELEPHONE: 313-965-1976
TELEPRAK: 313-965-1951
INPORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 33 anino acide
TYPE: anino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide
         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: N/A MOLECULE TYPE: PORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-152-488-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08436703B
Sequence 4, Application US/08436703B
Patent No. 5919761
GENERAL INFORMATION:
APPLICANT: Wakefield Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
ITLE OF INVENTION: HEPARIN AND LOW MOLECULAR;
ITLE OF INVENTION: WEIGHT HEPARIN
ITLE OF INVENTION: WIGHT HEPARIN
ITLE OF INVENTION: WAITCOAGULATION REVERSAL;
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benita J, Rohm, Esq.
STREET: 6601 Woodward Avenue
                                                                                        CURRENT APPLICATION DATA:

SOFTWARE: WordPerfect 6.1; ASCII (DOS) Text
CURRENT APPLICATION DATA:

FILING DATE: 08-SEPT-1994

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/06829

FILING DATE: 14-AUG-1992

APPLICATION NUMBER: PCT/US92/06829

FILING DATE: 12-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: ROAIM, BENITA 1.

TELEPHONE: 313-496-762

TELEPHONE: 313-496-9644

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 33 amino acid

TYPE: amino acid
    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy diskette 3.5" 1.44Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS V.6.22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AKKYAKK-EKAAKKAYKKEAKAKAAEAAKE 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Michigan
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , TITLE: N/A
; DOCUMENT NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993
US-08-303-025-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: WordPerfect 6;
SOFTWARE: ASCII (DOS) Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 48226
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: N/A
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Detroit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-436-703B-4
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Gaps

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Score 62.5; DB 1; Length 29;
Pred. No. 0.37;
1; Mismatches 9; Indels
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Sequence 10, Application US/08303025

Patent No. 5614494

GENERAL INFORMATION:
APPLICANT: Madefield, Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND TITLE OF INVENTION: ANTICOAGULATION REVERSAL
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benita J, Rohm, Esq.
STREET: 150 West Jefferson, Suite 2500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: STATE: MICHIGAN
COUNTRY: United States of America
ZIP: 49226-4415
ZIP: 49226-4415
ZIP: 49226-4415
ZOMPUTER: EADABLE FORM:
MEDIUM TYPE: Floppy diskette 3.5" 1.44Mb
COMPUTER: IBM FC Compatible
OPERATURG SYSTEM: MS-DOS v.6.22
OFFWARE: WordPerfect 6.1; ASCII (DOS) Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,025
FILING DATE: 08-SEPT-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/US92/06829
FILING DATE: 11-ANG-1993
APPLICATION NUMBER: DS 08/152,488
FILING DATE: 11-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: ROHM EBRICE/DOCKET NUMBER: 7WH-060548-00231
TELECOMMUNICATION INFORMATION:
METERCOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
METERCOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                            1 AKKYAKKEKAAKKAYKKEAKAKAAEAAAK 29
                                                                                                                                                                                                                                                                                                                                       2 AKKAAKKAKKAAKKAAK-KAKKAAKK 29
            AUTHORS: N/A
; TITLE: N/A
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993
US-08-152-488-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE: N/A
DOCUMENT NUMBER: PCT/US92/08069
                                                                                                                                                                                                              Query Match 37.7%;
Best Local Similarity 62.1%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; FILING DATE: 14-AUG-1993
US-08-303-025-10
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: N/A
    ORGANISM: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Detroit
STATE: Michiga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 37.7%; Score 62.5; DB 1; Length 29; Best Local Similarity 62.1%; Pred. No. 0.37; Matches 18; Conservative 1; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Wakefield, Thomas W.
APPLICANT: Madrews, Philip C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN TITLE OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTRY: New Jefsey
COMPUTRY: New Jefsey
COMPUTRY: United States of America
ZIP: 07016-1811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: NA-DOS
SOFTWARE: WORDER: WS-DOS
SOFTWARE: WORDER: US-NOV-1993
CLASSIFICATION NUMBER: US/08/152,488
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rohm, Benita J.
REGISTRATION NUMBER: Z8,664
REFERENCE/DOCKET NUMBER: RA-7MG
TELECOMMUNICATION INFORMATION:
TELEBHONE: 908-276-3344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AKKYAKKEKAAKKAYKKEAKAKAAEAAAK 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 AKKAAKKAAKKAAKKAAK-KAKKAAKK 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New Jersey
?: United States of America
                                                                                                                                                                                                                                                                             TITLE: N/A;
PUBLICATION INFORMATION:
DOCUMENT NUMBER: PCT/US92/08069;
FILING DATE: 14-AUG-1993
US-08-152-488-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Benita J, Rohm, Esq.
STREET: 512 Springfield Avenue
CITY: Cranford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11, Application US/08152488
Patent No. 5534619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS:
TELEFAX: 908-276-5543
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29 amino acids
                                                                                         TYPE: amino acid
STRANDEDNESS: N/A
TOPOLOGY: N/A
MOLECTLE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   908-276-5543
                                                                                                                                                                                                              ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: N/A
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: N/1
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US-08-152-488-11
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Gaps
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Best Local Similarity 62.1%; Pred. No. 0.37;
Matches 18; Conservative 1; Mismatches 9; Indels
                                                                                                                                                                   APPLICANT: Andrews, Philip C.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: NOVE PEPTIDES FOR HEPARIN AND TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN TITLE OF INVENTION: ANTICOAGULATION REVERSAL NUMBER OF SEQUENCES: 16 CORRESPONDENCE ADDRESS:
ADDRESSEE: Benita J, Rohm, Esq.
STREET: 150 West Jefferson, Suite 2500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-677-304-10
Sequence 10, Application US/08677304
Sequence 10, Application US/08677304
Sequence 10, Application US/08677304
SENERAL INFORMATION:
APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy diskette 3.5" 1.44Mb
COMPUTER: BEAPCH SALES OF AMERICA
COMPUTER: Floppy diskette 3.5" 1.44Mb
COMPUTER: WordPerfect 6.1; ASCII (DOS) Text
SOFTWARE: WordPerfect 6.1; ASCII (DOS) Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,025
FILING DATE: 08 -SEPT-1994
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/152,488
FILING DATE: 14-AUG-1992
APPLICATION NUMBER: US 08/152,488
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rohm, Benita J.
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRX: 313-496-8454
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARRATERISTICS:
LENGTH: 2.9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AKKYAKKEKAAKKAYKKEAKAKAAEAAAK 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Michigan
COUNTRY: United States of America
ZIP: 48226-4415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) DOCUMENT NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993
US-08-303-025-13
                                                                              Sequence 13, Application US/08303025
Patent No. 5614494
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
ORGANISM: N/A
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide
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STREET: LOC
TTW: Detroit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: TOPOLOGY: N/A MOLECULE TYPE: p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE: N/A
                                                   JS-08-303-025-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
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                                                                                     Gaps
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      37.7%; Score 62.5; DB 1; Length 29; larity 62.1%; Pred. No. 0.37; Conservative 1; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37.7%; Score 62.5; DB 1; Length 29; ilarity 62.1%; Pred. No. 0.37; Conservative 1; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James P.
TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN ITLE OF INVENTION: ANTICOAGULATION REVERSAL CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

REDIUM TYPE: Floppy diskette 3.5" 1.44Mb
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy diskette 3.5" 1.44Mb
COMPUTER: BM PC compatible
OPERATING SYSTEM: MS-DOS V.6.22
SOFTWARE: Wordberfect 6.1; ASCII (DOS) Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,025
FILING DATE: 08 SEPT-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/US92/06829
FILING DATE: 14-AUG-1992
APPLICATION NUMBER: US/08/152,488
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rohm, Benita J.
REFERRICE/DOCKET NUMBER: 7WH-060548-00231
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION TO THE TELECOMMU
                                                                                                                                           1 AKKYAKKEKAAKKAYKKEAKAKAAEAAAK 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Benita J, Rohm, Bag.
STREET: 150 West Jefferson, Suite 2500
                                                                                                                                                                                                            2 AKKAAKKAAKKAKKAAK-KAKKAAKK 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AKKYAKKEKAAKKAYKKEAKAKAAEAAAK 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Michigan : United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , IITLE: N/A
; DOCUMENT NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993
US-08-303-025-11
                                                                                                                                                                                                                                                                                                                                          US-08-303-025-11
; Sequence 11, Application US/08303025
; Patent No. 5614494
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 29 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PUBLICATION INFORMATION:
AUTHORS: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide
Query Match
Best Local Similarity
Matches 18; Conser
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Best Local Similarity
Matches 18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Detroit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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ij

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Search completed: June 3, 2005, 10:01:19 Job time: 42 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11, Application US/08677304
; Patent No. 5721212
; GENERAL INFORMATION:
APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
TITLE OF INVENTION: ANTICOAGULATION REVERSAL
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benita J, Rohm, Esq.
STREET: SIZ Springfield Avenue
CITY: Cranford
LOW MOLECULAR WEIGHT HEPARIN
ANTICOAGULATION REVERSAL
                                         NUMBER OF SECUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSE: Benita J, Rohm, Beq.
STRET: 512 Springfield Avenue
CITY: Cranford
STATE: New Jersey
COMPUTRY: United States of America
ZIP: 07016-1811
COMPUTRY: LBM PC Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORDPER: MS-DOS
SOFTWARE: WORDPER: US/OS/OS/TOXY
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/OS/677,304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AKKYAKKEKAAKKAYKKEAKAKAAEAAAK 29
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                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATE:

APPLICATION NUMBER: US/08/152,488

FILING DATE: 12-NOV-1933

APPLICATION NUMBER: US/08/152,488

FILING DATE: 14-AUG-1933

ATTORNEY/AGENT INPORMATION:

NAME: Rohm, Benita J.

REGISTRATION NUMBER: 28,664

REFERENCE/DOCKET NUMBER: 28,664

TELEFAX: 908-276-5543

INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTER.STICS: LENGTH: 29 amino acids

TYPE: amino acid STRANDEDNESS: NO: 5721212 Relevant

MOLECTUL TYPE: peptide

ORIGINAL SOURCE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PUBLICATION INFORMATION:
DOCUMENT NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 62.1
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: ·N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-677-304-10
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37.7%; Score 62.5; DB 1; Length 29; 62.1%; Pred. No. 0.37; tive 1; Mismatches 9; Indels
                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6; ASCII (DOS) Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/677,304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AKKYAKKEKAAKKAYKKEAKAKAAEAAAK 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 530
PRICING APPLICATION: 530
PRICOR PELICATION DATA:
PRILING DATE: 12.NOV-1993
APPLICATION NUMBER: US/08/152,488
FILING DATE: 14.AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rohm, Benita J.
REGISTRATION NUMBER: 28,664
REFERENCE/DOCKET NUMBER: RM-7WG
TELEPHONE: 908-276-3344
TELEPHONE: 908-276-5543
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
: New Jersey
RY: United States of America
07016-1811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: No. 5721212 Releva
TOPOLOGY: No. 5721212 Relevant
MOLBCTLE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: N/A
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE: N/A
PUBLICATION INFORMATION:
DOCUMENT NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 62.1
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

3, 2005, 10:09:37 ; Search time 38 Seconds
 (without alignments)
113.941 Million cell updates/sec June Run on:

US-10-792-311-2 Title: Perfect score:

213 1 AKKYAKKAKAEKAKKAYKAA......AKYEKAAAEKAAAKEAAYEA Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 45 Minimum DB Maximum DB Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

.. Database

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description					ō.	4.	antifreeze protein	homeotic protein u	antifreeze protein	dynein-associated	M24 protein - Stre	antifreeze protein	hypothetical prote	antifreeze protein	Balbiani ring 2 ch	photosystem I chai	ical	o	ubiquitin / riboso	ific	histone H3.2 - Tet	kinetoplast DNA-as	myosin regulatory	epsilon receptor m	nephritogenic prot	trifolitoxin precu			histone H3.2 - Tet
	ΙD	S10544	S04941	S10545	A05163	PT0028	A41270	A05162	S58853	FDF18G	S28908	A05112	FDF15G	F69800	FDFL3W	A24677	S23173	E89877	B24677	B40186	B45316	\$10263	D47256	A34594	A61220	A39124	A47116	T26815	S11416	S10267
	DB	2	7	7	N	~	~	~	7	H	~	~	Н	N	Ч	~	7	~	~	7	~	N	7	7	7	~	7	7	~	0
	Watch Length	45	45	45	45	44	32	33	40	40	39	35	33	36	37	35	38	44	35	32	35	41	22	36	18	42	42	44	20	41
مد	Match	27.7	27.7	27.2	26.8	26.1	23.0	22.5	22.5	21.8	21.4	20.4	19.7	ď	19.2		18.5	18.5	18.3	18.1	18.1	18.1	17.8	17.8	17.1	16.9	16.9	16.7	16.4	16.4
	Score	59	59	28	57	55.5	49	48	48	•	٠	٠	42	41.5	41	40	•	39.5	39	38.5	œ,	38.5	38	38	36.5		36		35	
1	No.		7	m	4	2	9	7	œ	6	10	11	12	13	14		16	17	18	19	20	21	22	23	24	25	26	27	28	29

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Gaps

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27.7%; Score 59; DB 2; Length 45; 48.6%; Pred. No. 22; tive 4; Mismatches 12; Indels

Query Match
Best Local Similarity 48.6
Matches 17; Conservative

1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEK 35

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7	histone H3.2 - Tet	H3.2 -	histone H3.2 - Tet	H3.2 -	H3.2 -	H3.2 -	histone H3.2 - Tet								
S10283	S10289	S10287	S10291	S10295	S10297	S10299	\$10285	S10259	S10261	S10265	S10269	S10271	S10273	S10275	S10277
N	~	C)	N	~	~	~	~	7	~	~	~	~	~	~	0
41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41
4	4.	6.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4
16.	16	_													
				35		35	35	35	32	32	35	32	35		32

ALIGNMENTS

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Protramine phi-3.2 - California mussel
NyAlternate names: protramine PL-1V.2
Signed as Wytilus californianus (California mussel)
Cippecies: Wytilus californianus (California mussel)
Cipate: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
Ribur J. Blochem. 182, 569-576, 1989
A;Title: Sequence and characterization of the sperm-specific protein phi3 from Mytilus of A;Reference number: S04941; MUID:89325302; PMID:2666130
A;Resion: S10544
A;Molecule type: protein
A;Residues: 1-45 Aus>
A;Coss-references: UNIPROT:P11860
C;Superfamily: histone H1
C;Keywords: DNA binding; nucleus
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NyAlternate names: protramine PL-IV.1
Cispecies: Myrilus californianus (California mussel)
Cispecies: Myrilus californianus (California mussel)
Cispecies: Myrilus californianus (California mussel)
Cipate: O'Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
Cipate: J. McParland, R.
RiAusio, J.; McParland, R.
Eur. J. Biochem. 182, 569-576, 1989
Airitle: Sequence and characterization of the sperm-specific protein phi3 from Mytilus of Airitle: Sequence and characterization of the sperm-specific protein Airitle: Sequence unber: S04941; MUD:89325302; PMID:2666130
Airitle: Sequence in S04941; MUD:89325302; PMID:2666130
Airitle: Source in S04941; MUD:89325302; PMID:2666130
Airitle: S04941; MUD:89325302; PMID:2666130
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Best Local Similarity 48.6'
Matches 17; Conservative
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R;Gusse, M.; Sautiere, P.; Chauviere, M.; Chevaillier, P.
Biochim. Biophys. Acta 748, 93-98, 1983
A;Title: Extraction, purification and characterization of the sperm protamines of the doc
A;Reference number: S01463; MUID:84000513; PMID:6615852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protamine S4 - smaller spotted catshark
NiAlternate names: scylliorhinine S4
C;Species Scylliorhinus canicula (smaller spotted catshark, smaller spotted dogfish)
C;Date: 27-Mar-1992 #sequence revision 27-Mar-1992 #text_change 09-Jul-2004
C;Accession: A41270; S12285
C;Accession: A41270; M: Briand, G; Martinage, A; Chevaillier, P.
Biochim. Biophys. Acta 791, 82-86, 1984
A;Title: Primary structure of scylliorhinine S4, a protamine isolated from sperm nuclei
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A;Reference number: A91150; MUID:85285003; PMID:4029130
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                                              Length 44;
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                                                                                                                                                                                                                                                                           | : :|| : | | : || : || | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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                                         DB 2;
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40.0%; Pred. No. 46;
:ive 10; Mismatches
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A;Residues: 1-5 <GUS>
C;Keywords: DNA binding; sperm; testis
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C, Superfamily: antifreeze protein
C, Keywords: antifreeze
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                                                                                                                            16; Conservative
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                                                                         Best Local Similarity
Matches 16; Conserva
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                                              Query Match
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A,Title: Identification of Leishmania genes encoding proteins containing tandemly repeat
A,Reference number: PT0027, MUID:88061089; PMID:3502718
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C,Species: Myoxocephalus scorpius (shorthorn sculpin, daddy sculpin)
C,Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                             N;Alternate names: protamine PL-IV.3
C;Species: Mytilus californianus (California mussel)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
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C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: PT0028
R;Wallis, A.E.; McMaster, W.R.
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R;Hew, C.L.; Joshi, S.; Wang, N.C.; Kao, M.H.; Ananthanarayanan, V.S. Eur. J Biochem. 151, 167-172, 1985
A;Title: Structures of shorthorn sculpin antifreeze polypeptides. A;Title: Atructures of shorthorn Sculpin antifreeze polypeptides. A;Title: Ap1150; MUID:85285003; PMID:4029130
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C;Superfamily: antifreeze protein
C;Keywords: antifreeze; blocked amino end; plasma
C;Keywords: antifreeze; blocked amino end; plasma
F;9-45/Region: alanine-rich
F;1/Modified site: blocked amino end (Met) #status experimental
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C,Superfamily: histone H1
C,Keywords: DNA binding; nucleus
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A; Residues: 1-44 < WAS>
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Query Match

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antifreeze protein GS-5 - grubby sculpin
C;Species: Myoxocephalus aenaeus (grubby sculpin)
C;Species: Myoxocephalus aenaeus (grubby sculpin)
C;Accession: S06417
R;Chakrabartty, A.; Hew, C.L.; Shears, M.; Fletcher, G.
Can. J. Zool, 66, 403-408, 1988
A;Title: Primary structures of the alanine-rich antifreeze polypeptides from grubby sculg
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Cipate: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
Cipate: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
Rixunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berterr C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
A,Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallerr isch, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.;
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A,Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y. M.; Ogawa, K.; Ogiwara, A.; Odiwara, A.; Odiwara, B.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A.; Althors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror, akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Togato, V.; Uchiyama,
                                                                                                                                                                                                                                             C;Species: Streptococcus pyogenes
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
C;Accession: A05112
F;Beachey, E.H.; Seyer, J.M.; Dale, J.B.; Hasty, D.L.
J. Biol. Chem. 258, 13250-13257, 1983
A;Reference number: A05112; MUID:84032558; PMID:6415061
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C;Superfamily: antifreeze protein
C;Keywords: antifreeze; blocked amino end
F;I/Modified site: blocked amino end (Met) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 19.7%; Score 42; DB 1; Length 33; Il Similarity 54.2%; Pred. No. 6.4e+02; 13; Conservative 1; Mismatches 10; Indels
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   2 AKEAKEALEAKERYMEEMADTADAIEMATLDKEMAEE
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                                                                                                                                                                                A05112
M24 protein - Streptococcus pyogenes (fragment)
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C;Superfamily: M5 protein
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Best Local Similarity
Matches 13; Conserva'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein A; Residues: 1-33 < CHA>
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R;Holzbaur, E.L.F.; Hammarback, J.A.; Paschal, B.M.; Kravit, N.G.; Pfister, K.K.; Vallee R;Holzbaur, E.L.F.; Hammarback, J.A.; Paschal, B.M.; Kravit, N.G.; Pfister, K.K.; Vallee A;Title 360, 695, 1992
A;Title Correction. Homology of a 150K cytoplasmic dynein-associated polypeptide with the A;Reference number: S28908; MUID:93101200; PMID:1361213
A;Accession: S28908
                                                                                                    C; Accession: S58853
R; Warren, R.W.; Nagy, L.; Selegue, J.; Gates, J.; Carroll, S.
Nature 372, 458-461, 1994
A; Title: Evolution of homeotic gene regulation and function in flies and butterflies.
A; Reference number: S58850; WUID:95075456; PMID:7840822
A; Accession: S58853
                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:025210; EMBL:L42137.
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1995 C;Superfamily: homeobox homology
C;Seywords: DNA binding; homeobox; nucleus; transcription regulation
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C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999
N;Alternate names: ultrabithorax homeodomain protein
C;Species: Junonia coenia
C;Date: 19-Mar_1997 #sequence_revision 29-Aug-1997 #text_change 16-Aug-2004
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                                                                                                                                                                                                                                                                                                          A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-40 <WAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 40;
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A;Residues: 1-40 <CHA>
A;Cross-references: UNIPROT:P20617
C;Superfamily: antifreeze protein
C;Keywords: antifreeze; blocked amino end
F;1/Modified site: blocked amino end (Met) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22.5%; Score 48; DB 2; Length 40; 50.0%; Pred. No. 2.1e+02; ive 4; Mismatches 8; Indels
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Best Local Similarity 50.0%
Matches 12, Conservative
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Best Local Similarity 40.59
Matches 15; Conservative
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A;Molecule type: mRNA
A;Residues: 1-39 <HOL>
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Search completed: June
Job time : 38 secs
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A;Experimental source: strain 168
C;Genetics:
A;Genetics:
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, I. A; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A;Reference number: A69580; MUID:98044033; PMID:9384377
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C;Species: Chironomus pallidivittatus
C;Species: Chironomus pallidivittatus
C;Bate: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 09-Jul-2004
C;Accession: A4677
R;Galler, R.; Saiga, H.; Widmer, R.M.; Lezzi, M.; Edstrom, J.E.
EMBO J. 4, 2977-2982, 1985
A;Tille: Two genes in Balbiani ring 2 with metabolically different 75S transcripts.
A;Reference number: A91023
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R;DeVries, A.L.; Lin, Y.
Biochim. Biophys. Acta 495, 388-392, 1977
A;Title: Structure of a peptide antifreeze and mechanism of adsorption to ice. A;Reference number: A03192; MUID:78060969; PMID:588591
A;Accession: A03192
                                                                                                                                                                    A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-36 <KUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antifreeze protein 3 - winter flounder
C;Species: Pseudopleuronectes americanus (winter flounder)
C;Date: 01-Sep_1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004
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Best Local Similarity 46.7%; Pred. No. 8.7e+02;
Matches 14; Conservative 1; Mismatches 15; Indels
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Best Local Similarity 35.3%; Pred. No. 7.7e+02;
Matches 12; Conservative 7; Mismatches 12;
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A;Residues: 1-35 cGAL-
A;Cress-references: UNIPROT:Q05463
C;Superfamily: unassigned Balbiani ring proteins
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A,Residues: 1-37 < DBV>
A,Cross-references: UNIPROT: P02733
C,Superfamily: antifreeze protein
C,Keywords: antifreeze
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Best Local Similarity
Matches 9; Conserv
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SEQUENCE FROM N.A.
STRAIN-HIDIOU) DSM 50701 / ATCC 15356 / NCIB 9529;
PubMed=14752164; DOI=10.1126/Bence.1093027;
PubMed=14752164; DOI=10.1126/Bence.1093027;
Rendulic S., Jagtap P., Robinus A., Eppinger M., Baar C., Lanz C.,
Keller H., Lambert C., Evans K.J., Goesmann A., Meyer F.,
Sockett R.E., Schuster S.C.;
A predator unmasked: life cycle of Bdellovibrio bacteriovorus from genomic perspective.";
Science 303:689-692(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bdellovibrio bacteriovorus.
Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
Bdellovibrionaceae; Bdellovibrio.
NCBI_TaxID=959;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OrderedLocusNames=Bd3800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                     PRELIMINARY;
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44 AA;
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les 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                  MCBI_TaxID=29397;
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
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NON TER
SEQUENCE
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                                                                      3, 2005, 10:01:26; Search time 171 Seconds (without alignments) 134.758 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                 1 AKKYAKKAKAEKAKKAYKAA......AKYEKAAAEKAAAKEAAYEA
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Q81fc5
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P02733
Q8p382
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                               1612378 segs, 512079187 residues
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ANP5 MYOAE
Q65RE2
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ANP3_PSEAM
Q8P382
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Q9DF18
PH13 MYTCA
ANP8 MYOSC
PRT4 SCYCA
ANP3 MYOSC
Q252I0
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Listing first 45 summaries
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Q818F4
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Match Length DB
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length: 45
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Maximum DB seq
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                  Ofte6 plasmodium (199949) nicotiana t Q7reb3 plasmodium (198813) shewanella (199718 staphylococ (1988) staphylococ (1988) staphylococ (199106 staphylosoc (199106 stap
xanthomonas
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Q8pel7
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Pred. No. 3.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lactobacillus delbrueckii (subsp. lactis).
Bacteria; Firmicutes; Lactobacillales; Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=ATCC 4797;
Langenheim J.F., Ulrich R.L.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF499145; AAQ66805.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAC365D7CFC6A162 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0711Y2;
0-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 KYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAK 39
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                       Q7RA66
Q9S9D9
Q7REB3
Q8SY3
Q9SY18
Q7A176
Q7A690
Q6G106
Q6G106
Q6G106
Q6G106
Q6G106
Q6G106
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000000000044444444
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Local Similarity
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                                                           SEQUENCE FROM N.A.
TISSUE=Skin;
                                                                                                                         42 AA;
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20-MAR-1987 (
05-JUL-2004 (
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ID PHI3 MYTCA
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PubMed=14671304; DOI=10.1126/science.1088727;
Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C., Heidelberg J.F., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J., Madupu R., Brinke C.M., Daugherty S.C., DeBoy R.T., Durkin A.S., Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J., Davidsen T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A. Weidman J.F., Khouri H.M., Feldblyum T.V., Utterback T.R., Wan Aken S.E., Lovoley D.R., Fraeser C.M.;
"Genome of Geobacter sulfurreducens: metal reduction in subsurface
                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Skin;
MEDLINE=21192197; PubMed=11136728; DOI=10.1074/jbc.M009293200;
Low W.-K., Lin Q., Stathakis C., Miao M., Fletcher G.L., Hew C.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Longhorn sculpin skin-type antifreeze protein.
Myoxocephalus octodecimspinosis (Longhorn sculpin).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Scorpaeniformes,
Cottoidei, Cottidae, Myoxocephalus.
                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
Geobacteraceae; Geobacter.
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                                                 DB 2; Length 43;
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Pred. No.'7.1;
                                                                         Indels
                                                                                                 1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAA 42
                                                                                                               2 AKKAAKKATKKAVKKTTKKV-AKKATKKVAKKATKKAA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35 AA; 3966 MW; 0E6E2B600A034777 CRC64;
                         43 AA; 4598 MW; 11AB9E005A80493C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                    Last annotation update)
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                                                                                                                                                                                                                         Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KKEEKKPVKKAKKAKKAKKEEKKEEAAAPAAEKK 35
                                                          Pred. No. 4.9;
2; Mismatches
                                                                                                                                                                                     35 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
                                                 Score 70.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete proteome; Hypothetical protein.
SEQUENCE 35 AA; 3966 MW; 0E6E2B600A0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                                                                            Created)
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EMBL; BX842656; CAE81160.1; -.
                                                 33.1%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31.9%;
                                                                                                                                                                                                        05-JUL-2004 (TEMBLEEL 27, 05-JUL-2004 (TEMBLEEL 27, Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 302:1967-1969(2003).
                                                                                                                                                                                                                                                        OrderedLocusNames=GSU3242;
                                                                                                                                                                                                                                                                      Geobacter sulfurreducens.
                                                          Local Similarity 50.0 tes 21; Conservative
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                                                                                                                                                                                     PRELIMINARY;
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            Complete proteome. SEQUENCE 43 AA:
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                                                                                                                                                                                                                                                                                                          NCBI TaxID=35554;
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                                                 Query Match
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Ausiou J., McDarland R.;

Ausiou J., McDarland R.;

"Sequence and characterization of the sperm-specific protein phi 3

I sequence and characterization of the sperm-specific protein phi 3

I was a sequence and characterization of the sperm-specific protein transition: histones

I was replaced by spermatid specific proteins which are themselves

Teplaced by protamines in late spermatids.

I will SUGELLANBOUS: The sequence of component I is shown.

I will SUG44; SUG44:

PIR; SUG44; SUG44:

R PIR; SIG44; SUG45.

R PIR; SIG45; SIG44:

R PIR; SIG45; SIG464:

W Nuclear protein; Nucleosome core; Spermatogenesis.

W Nuclear protein; Nucleosome core; Spermatogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              core; Spermatogenesis.

S -> T (possible variant of component I).

A -> T (in component II).

S -> T (possible variant of component I).

S -> T (possible variant of component I).

K -> R (in component III).

78A6BDF2CB7774BI CRC64;
                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Speri-specific protein Phi-3 (PL-IV).
Mytilus californianus (California mussel).
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
Mytiloidea; Mytilidae; Mytilus.
                                                                                                                                                                        Low W., Lin Q., Stathakis C., Miao M., Fletcher G.L., Hew C.L.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF306348; AAG22048.1; -.
"Isolation and characterization of skin-type, type I antifreeze polypeptides from the longhorn sculpin, Myoxocephalus octodecemspinosus.";
                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 59; DB 1; Length 45; Pred. No. 67;
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01-00T-1989 (Rel. 12, Created)
01-00T-1989 (Rel. 12, Last sequence update)
05-.TH.-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 04, Created)
(Rel. 04, Last sequence update)
(Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45 AA
                                                                                                                                                                                                                                                                                                                  ch 29.8%; Score 63.5; D
1 Similarity 53.8%; Pred. No. 23;
21; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 67;
4; Mismatches
                                                    J. Biol. Chem. 276:11582-11589(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=89325302; PubMed=2666130;
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17
18
39
4912 MW;
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                                                                                                                                                                                                                                                                   3796 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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MEDLINE=96223980; PubMed=8626748; DOI=10.1074/jbc.271.8.4106; Gong Z., Ewart K.V., Hu Z., Fletcher G.L., Hew C.-L.; Skin antifreeze protein genes of the winter flounder, Pleuronectes americanus, encode distinct and active polypeptides without the
                                                          20-MAR-1987 (Rel. 04, Created)
20-MAR-1987 (Rel. 04, Last sequence update)
20-MAR-1987 (Rel. 04, Last annotation update)
Antifreeze peptide SS-3.
Myoxocephalus scorpius (Shorthorn sculpin) (Daddy sculpin).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii, Neopterygii, Teleostei; Buteleostei; Neoteleostei;
Cottoidei; Cottidae; Myoxocephalus.
                                                                                                                                                                                                                                                                                                                                    Hew C.-L., Joshi S., Wang N.-C., Kao M.H., Ananthanarayanan V.S.;
"Structures of shorthorn sculpin antifreeze polypeptides.";
Eur. J. Biochem. 151:167-172(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95075456; PubMed=7840822; DOI=10.1038/372458a0; Warren R.W., Nagy L., Selegue J., Gates J., Carroll S.; "Evolution of homeotic gene regulation and function in flies and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ultrabithorax homeodomain protein (Fragment).
Junonia coenia (Peacock butterfly) (Precis coenia).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Paplilonoidea; Nymphalidae; Nymphalinae; Junonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22.5%; Score 48; DB 2; Length 42; 50.0%; Pred. No. 7.4e+02; ive 4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22.5%; Score 48; DB 1; Length 33; 51.4%; Pred. No. 5.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antifreeze protein; Direct protein sequencing; Repeat.
SEQUENCE 33 AA; 2939 MW; 8B74CC4C06A1208A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53C002E55430FE32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                       33 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47
                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                   MEDLINE=85285003; PubMed=4029130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; S58853; S58853.
GO; GO:0005634; C:nucleus; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L42137; AAA68463.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42 AA; 4380 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q25210;
01-NOV-1996 (TrEMBLrel. 01,
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                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 372:458-461(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
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                       MYOSC
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Q25210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sautiere P., Gusse M., Briand G., Martinage A., Chevaillier P., "Primary structure of scylliorhinine S4, a protamine isolated from sperm nuclei of the dog-fish Scylliorhinus caniculus.";

Blochim. Blophys. Acta 791:82-86 (1984).

-I- FUNCTION: Protamines substitute for histones in the chromatin of sperm during the haploid phase of spermatogenesis. They compact sperm DNA into a highly condensed, stable and inactive complex.

-I- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Chondrichthyes,
Elasmobranchii, Galeomorphii, Galeoidea, Carcharhiniformes,
Scyliorhinidae, Scyliorhinus.
Antifreeze peptide SS-8.

Myoxocephalus scorpius (Shorthorn sculpin) (Daddy sculpin).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;

Cottoidei; Cottidae; Myoxocephalus.
                                                                                                                                                                SEQUENCE.

MEDLINE=85285003; PubMed=4029130;

Hew C.-L., Joshi S., Wang N.-C., Kao M.H., Ananthanarayanan V.S.;

Hew C.-L., Joshi S., Wang N.-C., Kao M.H., Ananthanarayanan V.S.;

Structures of shorthorn sculpin antifreeze polypeptides.";

Eur. J. Biochem. 151:167-172(1985).

-!- FUNCTION: Antifreeze proteins lower the blood freezing point.

-!- SIMILARITY: Belongs to the type-I AFP family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A41270; A41270.
Chromosomal protein; Direct protein sequencing; DNA condensation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA-binding; Nuclear protein; Nucleosome core; Spermatogenesis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                    PIR; A05163; A05163.
Antifreeze protein; Direct protein sequencing; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                            4006 MW; 260C0BCC663B6878 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32 AA; 3882 MW; 4C4E9F58958D1AEF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26.8%; Score 57; DB 1; 1 56.2%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-APR-1993 (Rel. 25, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 KKAYKAAEAKKAAKYEKAAAEKAAAKEAAYEA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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Matches 18; Conservative
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Les 12; Conserv
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SEQUENCE Query Match

Matches

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PRT4 SCYCA

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Matches

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Query Match

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SEQUENCE FROM N.A.

MEDLINES91010200; PubMed=1361213; DOI=10.1038/360695a0;

MEDLINES93010200; PubMed=1361213; DOI=10.1038/360695a0;

Holzbaur E.L., Hammarback J.A., Paschal B.M., Kravit N.G.,

Pfister K.K., Vallee R.B.;

"Homology of a 150K cytoplasmic dynein-associated polypeptide with the Drosophila gene Glued.";

Drosophila gene Glued.";

Nature 360:695-695(1992).
                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582; Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B., Kapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A., Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T., Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D., "Genome sequence of Bacillus cereus and comparative analysis with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i-SIMILARITY: Belongs to the S21P family of ribosomal proteins. BEL1, ABO17012; APP12220.1; -. G0; G0:0005840; C:ribosome; IEA. G0; G0:0003735; P:structural constituent of ribosome; IEA. G0; G0:0006412; P:protein biosynthesis; IEA. Interpro; IPR001911; Ribosomal_S21. Feather PF01165; Ribosomal_S21; I.
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1 Similarity 40.5%; Pred. No. 1.2e+03;
15; Conservative 5; Mismatches 16; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39 AA; 4478 MW; 3790810EA5AB2F7C CRC64;
                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 AKKAK-AEKAKKAYKAAEAKKAAKYEKAAAEKAAAKE 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus cereus (strain ATCC 14579 / DSM 31).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 AEAKKAAKYEKAAAEKAAAKEAA 42
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                                                                                                                         P150GLUED=GLUED homolog (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10; Conservative
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Best Local Similarity
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SEQUENCE
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Q818F4
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"Primary structures of the alamine-rich antifreeze polypeptides from grubby sculpin, Myoxocephalus aenaeus.";
Can. J. Zool. 66:403-408(1988).
-!- FUNCTION: Antifreeze proteins lower the blood freezing point.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTOR STANDARD; PRT; 40 AA.

P20617;
01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1991 (Rel. 17, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
05-JUL-2004 (Rel. 44, Last annotation update)
Myoxocephalus aenaeus (Grubby sculpin).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes; Cottoidei; Cottidae; Myoxocephalus.
                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22.1%; Score 47; DB 2; Length 42; 47.8%; Pred. No. 9.3e+02; Live 2; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yang J.-Y., Wang Y.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF271256; AAKS8397.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antifreeze protein; Direct protein sequencing; Repeat. MOD RES 1 1 Blocked amino end (Met). SEQUENCE 40 AA; 3579 MW; 32F50BE243C2AD11 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42 AA; 5559 MW; 52CDCC6AADF9C2FB CRC64;
                                                                                                                                                                                                                                                                                                                                                  annotation update)
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                                                                                                                                                                                                                                                                                                                    Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42
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                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence upo
01-DCT-2002 (TrEMBLrel. 22, Last annotation upo
HBV presi(21-47) binding protein (Fragment).
                                                                                                                                                                                                                        42 AA.
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21 EAKKAAKYEKAAAEKAAAKEAAYE 44
                                                              EQEKQAQAQKAAAAAAAAAAQD 38
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                                                                                                                                                                                                                        PRT;
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les 11; Conservative
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Matches

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Gaps

RESULT 12

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MEDLINE=22608306; PubMed=12692562;
Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T., Sakaki Y., Hattori M., Omura S.;
"Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis.";
Nat. Biotechnol. 21:526-531(2003).
EMBL: AP05037; BACTIT67.1;
Complete proteome; Hypothetical protein.
SEQUENCE 44 AA; 4867 MW; 435C4EBIBBF3A577 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bebear C.M., Charron A., Bove J.M., Bebear C., Renaudin J.;
"Cloning and nucleotide sequences of the topolsomerase IV parC and
parE genes of Mycoplasma hominis.";
Antimicrob. Agents Chemother. 42:2024-2031(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Mycoplasma hominis.
Mycoplasma Pirmicutes; Mollicutes; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                               MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198; MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198; Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C., Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T., Kikuchi H., Shiba T., Sakaki Y., Hattori M.; "Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary metabolites."
                                                                                                                                         Streptomyces avermitilis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=PG21;
Bebear C.M., Charron A., Bove J.M., Bebear C., Renaudin J.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF036961; AAC33843.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 45; DB 2; Length 44;
Pred. No. 1.5e+03;
6; Mismatches 11; Indels
                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001)
                                                                                                                                                                        Streptomycineae; Streptomycetaceae; Streptomyces
                               44 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37 AA.
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                                                             Created)
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                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21.1%;
                                                         01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                        Hypothetical protein.
OrderedLocusNames=SAV4055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 39.3
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                               PRELIMINARY;
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                       NCBI_TaxID=33903;
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                               Q82G43
RESULT 14
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                Q82G43
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

3, 2005, 10:00:36; Search time 157 Seconds (without alignments) 110.855 Million cell updates/sec

US-10-792-311-2 213 Perfect score:

1 AKKYAKKAKAEKAKKAYKAA......AKYEKAAAEKAAAKEAAYEA Sequence:

45

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

2105692 seqs, 386760381 residues Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 45 Minimum DB E Maximum DB E Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_16Dec04:* geneseqp1980s:* Database

geneseqp1990s:*

geneseqp2003as:* geneseqp2003bs:* geneseqp2000s:* geneseqp2001s:* geneseqp2002s:*

geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		de					
Result No.	Score	Query Match	Query Match Length	DB	ID	Description	c
-	213	100.0	45	۳.	AAY82572	Aay82572 Co	Copolymer
7	108	50.7	35	m	AAY82571	Aay82571 Co	Copolymer
٣	86	40.4	39	~	AAW44934		Mycobacte
4	98	40.4	39	7	ADF45561	Adf45561 Me	Methylate
'n	74.5	35.0	32	~	AAR90180	Aar90180 Po	Polycatio
9	74.5	35.0	32	~	AAW06686		Protamine
7	74.5	35.0	33	~	AAR90181	Aar90181 Po	Polycatio
8	74.5	35.0	33	~	AAW06688	Aaw06688 Pr	Protamine
6	74	34.7	40	m	AAB08170	Aab08170 Pe	Peptide m
10	72	33.8	29	~	AAR90178	Aar90178 Po	Polycatio
11	72	33.8	29	~	AAR90176	Aar90176 Po	Polycatio
12	72	33.8	29	~	AAW06687	Aaw06687 Pr	Protamine
13	72	33.8	7	٩	AAW06697	Aaw06697 Pr	Protamine
14	69	32.4	e	m	AAB08175	Aab08175 Pe	Peptide m
15	68	31.9	36	m	AAB08169	Aab08169 Pe	Peptide m
16	67	31.5	28	7	AAR90177	Aar90177 Po	Polycatio
17	67	31.5	28	~	AAW06685	Aaw06685 Pr	Protamine
18	67	31.5		~	AAW22872	Aaw22872 P.	. americ
19	66.5	31.2	42	æ	AD043175	Ado43175 Pe	Peptide u
20	99	31.0	29	7	AAR90179	Aar90179 Po	Polycatio
21	99	31.0	8	~	AAW06698	Aaw06698 Pr	Protamine
22	64	30.0	٣	7	AAW22868	Aaw22868 P.	. americ
23	64	30.0	e	m	AAY44714	Aay44714 Wi	Winter fl
24	63.5	29.8	32	m	AAB08168		Peptide m
25	63	29.6	42	4	AA009072	Aa009072 Hu	Human pol

	Aaw52875 Nucleic a Aaw65937 Histone b Aaw69208 Nucleic a Aaw24450 Nucleic a		Aau04283 Trimeric Aaw2281 P. americ Aaw22876 Synthetic Aab08167 Peptide m	Ado43177 Peptide u Ado43181 Peptide u Aaw38224 NBC11 pep	Adn11701 Peptide l Aaw38892 Delivery Aaw38893 Delivery
AAW08398 AAW08396 AAW38228	AAW52875 AAW65937 AAW69208 AAW34450	AAY98493 AAY59038 AAB45846	AAU04283 AAW22881 AAW22876 AAB08167	ADO43177 ADO43181 AAW38224	ADN11701 AAW38892 AAW38893
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29.3 29.3	2000	29.1 29.1 29.1	29.1 28.6 28.6 28.6	28.2 28.2 27.9	27.9 27.7 27.7
62.5 62.5	62.5 62.5 62.5	6222 6222 6222	62 61 61 60.5	60 60 59.5	59.5 59 59
	310	3 3 3 1 5 4 3	333 34 36 36	0 4 4 4 0 1 2	44 44 5

ALIGNMENTS

AAY82572

AAY82572 standard; peptide; 45 AA.

(first entry) 28-JUL-2000

Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:2.

Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyalinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; permphigus vulgaris; systemic lupus erythematosus.

Unidentified

WO200018794-A1.

99WO-US022402. 24-SEP-1999; 98US-0101693P. 25-SEP-1998; (YEDA) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.

Lis D; Gad A,

WPI; 2000-317499/27.

Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.

Claim 10; Page 14; 72pp; English.

AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides

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treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include arthritic conditions, demyeliated for antibody-mediated diseases and include arthritic conditions, demyeliating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid attributits, osteoarthritis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune thyroiditis, autoimmune uveoretinitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxodedma, mysathenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated mediated diseases which can be treated include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The properties of the invention have defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as molecular weight markers
are used as molecular weight markers for glatiramer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 45 AA;
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Gaps
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100.0%; Score 213; DB 3; Length 45; 100.0%; Pred. No. 3.4e-16; ive 0; Mismatches 0; Indels
                                                                               1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAAYEA 45
                                       45; Conservative
Query Match
Best Local Similarity
Matches 45; Conserv
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1 AKKYAKKAKAKAEKAKKAYKAAEAKKAAKKAKYEKAAAKEAAAKEAAYEA 45

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RESULT 2 AAY8257

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AAY82571 standard; peptide; 35 AA.

28-JUL-2000 (first entry) AAY82571;

Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:1.

antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus. glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; Copolymer; molecular weight marker; TV-marker; immune disease;

Jnidentified

WO200018794-A1.

36-APR-2000.

99WO-US022402. 24-SEP-1999; 98US-0101693P. 25-SEP-1998;

(YEDA) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.

3ad A, Lis D;

WPI; 2000-317499/27.

Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases

Claim 10; Page 14; 72pp; English

AAY82571 to AAY82577 represent specifically claimed copolymer molecular

This peptide represents a fragment of a surface protein found on

Claim 5; Page 35; 52pp; French.

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investion describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer acta content of the invention are used as molecular weight markers for glatiramer actate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases such diseases include arthritic conditions, demyelinating arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune carbitis, autoimmune throughly autoimmune uveoretinitis, contact sensitivity disease, diabetes mellitus, Graves disease, dilabin-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, sporiasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated mediated diseases which can be treated include host-versus-graft disease, and delayed-type hypersensitivity. The mediated disease, and delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New peptide(s) involved in adhesion of mycobacteria to epithelial cells -
used in vaccines and for diagnosing mycobacterial infection, also use of
sulphated saccharide(s) and glyco-conjugate(s) to prevent mycobacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Surface protein, Mycobacterium bovis; BCG; adhesion; epithelium; Bacille Calmette-duerin; Mycobacterium tuberculosis; epithelial cell; heparin-binding haemagglutinin antigen; PCR; primer; amplification; probe; hybridisation; chromosome; vaccine; diagnosis; immunoassay.
                                                                                                                                                                                                                                                                                                                                                                                               properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as molecular weight markers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterial heparin-binding haemagglutinin antigen peptide fragment
weight TV-marker polypeptides from the present invention. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.7%; Score 108; DB 3; Length 35; 64.4%; Pred. No. 6.8e-05; ive 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AKKYAKKAKAKERAKKAYKAAEAKKAAKYEKAAAEKAAAKEAAYEA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (INSP ) INST PASTEUR LILLE.
(INRM ) INST NAT SANTE & RECH MEDICALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW44934 standard; peptide; 39 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97WO-FR000886.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-018517/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 35 AA;
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microorganisms over a Heparin-Sepharose column and eluting proteins with a gradient of 0.0.5 M NaCl. Fractions were separated by gel electrophoresis and a 28 kb heparin binding protein purified. N-terminal and internal peptide fractions were sequenced and the amino acid sequences used to design PCR primers. These amplified a 150 bp fragment (AAT76947) used as a probe to isolate chromosomal fragments containing the gene (AAT76948). The gene encodes a protein which is a heparinbinding haemagglutinin antigen (HBHA). The peptide can be used in tuberculosis), or can be used to diagnose mycobacterial infections of tuberculosis), or can be used to diagnose mycobacterial infection (by immunoassay detection of anti-HBHA antibodies) Mycobacterium bovis BCG (Bacille Calmette-Guerin) or M. tuberculosis, which enable mycobacteria to adhere to host, especially epithelial, cells. The antigen was isolated by passing a culture of BCG

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Sequence 39 AA;

Length 39; 7; Indels DB 2; 0.019; 11 EKAKKAYKAAEAKKAAKYEKAAAEKAAKEAA 42 Score 86; DB 2 Pred. No. 0.019 4; Mismatches 40.4%; 21; Conservative Similarity Query Match Best Local S Matches Š

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Gaps ö

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RESULT 4

ADF45561 standard; peptide; 39 AA ADF45561;

12-FEB-2004 (first entry)

vaccine; immunogen; methylation; heparin-binding hemagglutinin antigen; Mycobacterium bovis; Mycobacterium tuberculosis. Methylated HBHA peptide for vaccine against mycobacterial infections.

Mycobacterium sp

FR2832410-A1

23-MAY-2003.

19-NOV-2001; 2001FR-00014953

19-NOV-2001; 2001FR-00014953

New poly:cationic polypeptide n-protamine analogues - having reduced cationic charge and lower toxicity, used for reversing (low mol.wt.) heparin anticoagulation.

Disclosure; Page 13; 34pp; English.

(INSP) INST PASTEUR LILLE. (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

Locht C; Menozzi F, Pethe K,

WPI; 2003-471775/45.

New recombinant methylated mycobacterial heparin-binding hemagglutinin, useful as immunogen in anti-tuberculosis vaccines, also vectors for its Disclosure; Fig 2; 41pp; French. preparation.

The invention relates to an immunogenic recombinant peptide which is the methylated form of an expression product of a nucleic acid that encodes a mycobacterial heparin-binding hemagglutinin antigen (HBHA), especially from Mycobacterium bovis BCG or M.tuberculosis. The peptide, also methylated native HBHA, is used to prepare vaccines against mycobacterial peptide is the carboxyterminal of HBHA which binds to heparin. Methylation of this peptide occurs on the side chains of the lysine amino acids with either a methyl or dimethyl group.

Sequence 39 AA;

Sequence 32 AA;

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               Gaps
                                                                                                                                     n-protamine; anticoagulation reversal; low molecular weight heparin; polycationic; positively charged amino acid; lysine.
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Length 39;
              7; Indels
                                                                                                                                                                                                      /note= "C-terminal is in amide form"
                                                                                                                                                                                        note= "N-terminal is acetylated"
Score 86; DB 7;
Pred. No. 0.019;
4; Mismatches
                                                                                                                        Polycationic polypeptide n-protamine analogue
                             11 EKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAA 42
                                    Andrews PC;
                                                                                                                                                                          Location/Qualifiers
                                                                              AAR90180 standard; peptide; 32
                                                                                                                                                                                                                                                 94WO-US012981.
                                                                                                                                                                                                                                                              93US-00152488.
94US-00303025.
 40.4%;
                                                                                                                                                                                                                                                                                                  Wakefield TW, Stanley JC,
                                                                                                          (first entry)
               21; Conservative
                                                                                                                                                                                                                                                                                    (UNMI ) UNIV MICHIGAN
        Similarity
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Modified-site
                                                                                                                                                                                               Modified-site
                                                                                                          25-MAR-1996
                                                                                                                                                                                                                     W09513083-A1
                                                                                                                                                                                                                                                 10-NOV-1994;
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                                                                                                                                                                                                                                  18-MAY-1995
                                                                                                                                                            Synthetic.
Query Match
Best Local S:
Matches 21,
                                                                                           AAR90180;
                                                                        AAR90180
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Novel peptides are claimed which contain 20-40 amino acids and which have a total cationic charge of less than +21 (pref. +16 to +18; esp. +18) as determined by the number of positively charged amino acids in the sequence. Preferably the positive harges are grouped in clusters sequence. Preferably the positive harges are grouped in clusters amino acids having blocks of 2-4 positively charged amino acids separated by blocks of 2-6 neutral acids. Alternatively the positive charge may be distributed evenly or randomly along the peptide sequence. In particular the peptides are analogues of n-protamine (total cationic charge = +21) in which selected arginine residues have been replaced with uncharged amino acids and other arginine residues have been replaced by other positively charged amino acid residues, preferably lysine. The peptides reverse the effect of low mol. Wt. heparin (LMWH) anticoagulation and chence can be used medically to prevent bleeding after the conclusion of clinical procedures using heparin therapy. They are less toxic than n-protamine since the reduced positive charge gives an improved efficiency to toxicity ratio, and they may be more effective than n-protamine in their anti-LMWH action. The present sequence (total cationic charge = +18) is a specific example of the new polypeptides

Length 32;

Sequence 32 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protamine sulphate (also called n-protamine or salmine protamine) is a polycationic peptide derived from salmon sperm and is used to reverse heparin anticoagulation. One of the major components of salmine protamine is a 32 amino acid peptides of 20-40 amino acids of 1-21, with arginine accounting for 67% of the total sequence and for all of the positive charge. Peptides of 20-40 amino acids with total cationic charge less than [+21] and which are able, at least partially, to reverse the effect of heparin and/or low molecular weight heparin anticoagulants are effect of heparin and/or low molecular weight heparin anticoagulants are protamine where the positive charge on the amino acid sequence is reduced by selective replacement of positively charge on the amino acid sequence is reduced by selective replacement total cationic charge is less than [+21]. The uncharged residue, so that total cationic charge is less than [+21]. The have the same anti-heparin activity as protamine but are less toxic the cause of the reduced number of positive charges) and are relatively
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                                                                                                                                                                                                                                                   Coagulation, anticoagulant; heparin; platelet aggregation; cell adhesion; positively charged cluster; arginine; polycationic; decrease; n-protamine; salmine protamine; protamine sulphate; salmon sperm.
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/label= repeat region
/note= "4 tandem repeats of (Lys)2(Ala)2(Lys)2Ala motif"
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide reversing the anticoagulant effects of heparin - is based on protamine but has fewer positive charges for reduced toxicity.
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             Length 32;
                                    Indels
                                     4;
             DB 2;
             Score 74.5; DB Pred. No. 0.27; 3; Mismatches
                                                             5 AKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKA 36
                                                                                    AKKA-AKKAKKA--AKKAKKAAKKAKKA 30
                                                                                                                                                                                                                             Protamine-like peptide analogue [+18B].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Andrews PC;
                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                      note= "acetylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 5; 42pp; English.
                                                                                                                                                    AAW06686 standard; peptide; 32 AA
                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "amidated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96WO-US006567.
           Query Match 35.0%;
Best Local Similarity 68.8%;
Matches 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stanley JC,
                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                             Key
Modified-site
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                                                                                                                                                                                                    05-AUG-1997
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                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                           AAW06686;
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ID AAW0
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Novel peptides are claimed which contain 20-40 amino acids and which have a total cationic charge of less than +21 (pref. +16 to +18; esp. +18) as determined by the number of positively charged amino acids in the sequence. Preferably the positive charges are grouped in clusters sequence. Preferably the positive charges are grouped in clusters sequence. Preferably the positive of charges are grouped in clusters amono acids having blocks of 2-4 positively charged amino acids separated by blocks of 2-6 neutral acids. Alternatively the positive charge may be distributed evenly or randomly along the peptide sequence. In particular the peptides are analogues of n-protamine (total cationic charge = +21) the peptides are analogues of n-protamine (total cationic charge = +21) amino acids and other arginine residues have been replaced by other positively charged amino acid residues, preferably lysine. The peptides cannon acid residues have been replaced by other positively charged amino acid residues, preferably lysine. The peptides charge the effect of low mol. Wt. heparin (LMMH) anticoagning and charge gives an improved efficiency to contacty ratio; and they may be more effective than n-protamine in their anti-LMMH action. The present sequence (total cationic charge = 16) is a specific example of the new polypeptides
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                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              n-protamine; anticoagulation reversal; low molecular weight heparin; polycationic; positively charged amino acid; lysine.
                                                                     3;
                                                                     4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "C-terminal is in amide form"
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Score 74.5; DB 2;
Pred. No. 0.27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polycationic polypeptide n-protamine analogue
                                                                                                                                                                                  2 AKKA-AKKAKKA-AKKAKKAAKKAAKKA 30
                                                                                                                                        5 AKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKA 36
                                                                     3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                           AAR90181 standard; peptide; 33
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94US-00303025.
35.0%;
68.8%;
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                                                                     22; Conservative
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protamine sulphate (also called n-protamine or salmine protamine) is a polycationic peptide derived from salmon sperm and is used to reverse topolycationic opeptide derived from salmon sperm and is used to reverse is a 32 amino acid peptide having a total cationic charge of [421], with carginine accounting for 67% of the total sequence and for all of the positive charge. Peptides of 20-40 amino acids with total cationic charge less than [421] and which are able, at least partially, to reverse the effect of heparin and/or low molecular weight heparin anticoagulants are claimed. Specifically, the peptides are polycationic analogues of n-cromanie where the positive charge on the amino acid sequence is reduced by selective replacement of positively charged arguine residues with an uncharged residue, so that total cationic charge is less than [421]. The new peptides are used in vivo to reverse the effects of heparin; they have the same anti-heparin activity as protamine but are less toxic (because of the reduced number of positive charges) and are relatively easy and inexpensive to prepare. The present sequence represents a specific example of a protamine-like peptide with a charge of [+18] which
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                                                                                                                                                                                                                                                                   Coagulation, anticoagulant; heparin; platelet aggregation; cell adhesion; positively charged cluster; arginine; polycationic; decrease; n-protamine; salmine protamine; protamine sulphate; salmon sperm.
                                                                                                                                                                                                                                                                                                                                                                                              /label= repeat_region
/note= "4 tandem repeats of (Lys)2(Ala)2(Lys)2Ala motif"
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide reversing the anticoagulant effects of heparin - is based on protamine but has fewer positive charges for reduced toxicity.
                                                          3,
                                   Length 33;
                                                          Indels
                                  5; DB 2;
0.28;
                                                          4
                                                                                5 AKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKA 36
                                                                                            .3 AKKA-AKKAKKA--AKKAKKAAKKAAKKA 31
                                 Score 74.5; Di
Pred. No. 0.28
3; Mismatches
                                                                                                                                                                                                                                            Protamine-like peptide analogue [+18BE].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stanley JC, Andrews PC;
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                                                                                                                                                                   AAW06688 standard; peptide; 33
                                 35.0%;
68.8%;
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                                                         22; Conservative
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/label=
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                                 Query Match
Best Local Similarity
          Sequence 33 AA;
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                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                             AAW06688;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel synthetic peptides with high affinity for glycoaminoglycans and proteoglycans, useful for modulating heparin, promoting cell attachment, modulating tumor metastasis and modulating wound healing.
has been found to reverse the anticoagulation effects of both standard and low molecular weight heparin
                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoaminoglycan; proteoglycan; heparin modulation; anticoagulant;
cell attachment; cell adhesion; vein graft; tumour cell metastasis;
cartilage differentiation; wound healing.
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                                                                                                                                             Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide modulating activity of heparin, and other glycans.
                                                                                                                                                                                                   4; Indels
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                                                                                                                                          35.0%; Score 74.5; DB 68.8%; Pred. No. 0.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB08170 standard; peptide; 40 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-FEB-2000; 2000WO-US002853.
                                                                                                                                                                     68.8%;
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nes 21; Conservative
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                                                                                                                                                                        Similarity
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                                                                                     Sequence 33 AA;
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Best Local 8
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1 ARKKAAKAARKKAAKAAR----KKAAKAARKKAAKAARKKAA 38

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Fri Jun

New poly:cationic polypeptide n-protamine analogues - having reduced cationic charge and lower toxicity, used for reversing (low mol.wt.) n-protamine; anticoagulation reversal; low molecular weight heparin; polycationic; positively charged amino acid; lysine. /note= "C-terminal is in amide form" 'note= "N-terminal is acetylated" Polycationic polypeptide n-protamine analogue. 33.8%; Score 72; DB 2; 72.4%; Pred. No. 0.46; cive 2; Mismatches ; Stanley JC, Andrews PC; Location/Qualifiers Disclosure; Page 13; 34pp; English. AAR90178 standard; peptide; 29 AA. 94WO-US012981. 93US-00152488. (first entry) neparin anticoagulation. (UNMI) UNIV MICHIGAN WPI; 1995-193899/25. Sequence 29 AA; Wakefield TW, Modified-site Modified-site 10-NOV-1994; WO9513083-A1 12-NOV-1993; 38-SEP-1994; 25-MAR-1996 18-MAY-1995 Synthetic AAR90178; Query Match RESULT 10

Novel peptides are claimed which contain 20-40 amino acids and which have a total cationic charge of less than +21 (pref. +16 to +18; esp. +18) as determined by the number of positively charged amino acids in the sequence. Preferably the positive charges are grouped in clusters separated by neutral amino acids. Especially the peptides contain 28-32 amino acids having blocks of 2-4 positively charged amino acids separated by blocks of 2-6 neutral acids. Alternatively the positive charge may be distributed evenly or randomly along the peptide sequence. In particular the peptides are analogues of n-protamine (total cationic charge = +21) in which selected arguine residues have been replaced with uncharged amino acids and other arguine residues have been replaced by other positively charged amino acid residues, preferably lysine. The peptides reverse the effect of low mol. wt. heparin (LMMH) anticoagulation and clanced medically to prevent bleeding after the conclusion of clinical procedures using heparin therapy. They are less toxic than n-permine since the reduced positive charge gives an improved efficiency to toxicity ratio; and they may be more effective than n-protamine in their anti-LMWH action. The present sequence (total cationic charge = +16) is a specific example of the new polypeptides

1 AKKYAKKAK--AEKAKKAYKAAEAKKAAK 27 Conservative Similarity 21; Local Matches

New poly:cationic polypeptide n-protamine analogues - having reduced cationic charge and lower toxicity, used for reversing (low mol.wt.) n-protamine, anticoagulation reversal, low molecular weight heparin, polycationic, positively charged amino acid, lysine. /note= "C-terminal can be in amide form" 'note= "N-terminal can be acetylated" Polycationic polypeptide n-protamine analogue. 2 AKKAAKKAKKAAKKA--AKKAKKAAK 28 Wakefield TW, Stanley JC, Andrews PC; Location/Qualifiers AAR90176 standard; peptide; 29 AA. 94WO-US012981. 93US-00152488. 94US-00303025. (first entry) (UNMI) UNIV MICHIGAN, WPI; 1995-193899/25. Modified-site Addified-site 10-NOV-1994; WO9513083-A1 12-NOV-1993; 08-SEP-1994; 25-MAR-1996 18-MAY-1995. Synthetic. AAR90176; RESULT 11 AAR90176 셤

heparin anticoagulation.

Disclosure; Page 13; 34pp; English.

Novel peptides are claimed which contain 20-40 amino acids and which have

a total cationic charge of less than +21 (pref. +16 to +18; esp. +18) as

determined by the number of positively charged amino acids in the

sequence. Preferably the positive charges are grouped in clusters

ceparated by neutral amino acids. Especially the peptides contain 28-32

amino acids having blocks of 2-4 positively charged amino acids separated

by blocks of 2-6 neutral acids. Alternatively the positive charge may be

cistributed evenly or randomly along the peptide sequence. In particular

the peptides are analogues of n-protamine (total cationic charge = +21)

the peptides are analogues of n-protamine (total cationic charge = +21)

continued selected arginine residues have been replaced by other

continued and other arginine residues have been replaced by other

continued and other arginine residues have been replaced by other

continued procedures using heparin (LMMH) anticoagulation and

chance can be used medically to prevent bleeding after the conclusion of

clinical procedures using heparin therapy. They are less toxic than n
continued the reduced positive charge gives an improved efficiency

to toxicity ratio; and they may be more effective than n-protamine in

chair anti-LMMH action. The present sequence (total cationic charge =

total anti-LAMH action. The present sequence (total cationic charge =

total cationic charge =

total

Sequence 29 AA;

Gaps 4; 33.8%; Score 72; DB 2; Length 29; 72.4%; Pred. No. 0.46; ive 2; Mismatches 2; Indels Best_Local Similarity 72.4%; Matches 21, Conservative Query Match

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1 AKKYAKKAK--AEKAKKAYKAAEAKKAAK 27

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Gaps

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Length 29; Indels

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claimed. Specifically, the peptides are polycationic analogues of norotamine where the positive charge on the amino acid sequence is reduced by selective replacement of positively charged arginine residues with an uncharged residue, so that total cationic charge is less than [+21]. The new peptides are used in vivo to reverse the effects of heparin; they have the same anti-heparin activity as protamine but are less toxic (because of the reduced number of positive charges) and are relatively easy and inexpensive to prepare. The present sequence represents a specific example of a protamine-like peptide with a charge of [+16] which has been found to reverse the anticoagulation effects of both standard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protamine sulphate (also called n-protamine or salmine protamine) is a polycationic peptide derived from salmon sperm and is used to reverse heparin anticoagulation. One of the major components of salmine protamine is a 32 amino acid peptide having a total cationic charge of [+21], with arginine accounting for 67% of the total sequence and for all of the positive charge. Peptides of 20-40 amino acids with total cationic charge less than [+21] and which are able, at least partially, to reverse the effect of heparin and/or low molecular weight heparin anticoagulants are
                                                                                                                                                                                                                                     Coagulation; anticoagulant; heparin; platelet aggregation; cell adhesion; positively charged cluster; arginine; polycationic; decrease; n-protamine; salmine protamine; protamine sulphate; salmon sperm.
                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "4 tandem repeats of Ala(Lys)2(Ala)2(Lys)2 motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide reversing the anticoagulant effects of heparin - is based on protamine but has fewer positive charges for reduced toxicity.
2 AKKAAKKAKKAKKA--AKKAKKAAK 28
                                                                                                                                                                                                  Protamine-like peptide analogue [+16BE]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stanley JC, Andrews PC;
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/label= repeat_region
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                                                                                                                                                                                                                                                                                                                                                                                         'note= "acetylated"
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                                                                                        AAW06687 standard; peptide; 29 AA
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                                                                                                                                                                 (first entry)
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Modified-site
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                                                                                                                                                                                                                                                                                                                  Synthetic
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Protamine sulphate (also called n-protamine or salmine protamine) is a polycationic peptide derived from salmon sperm and is used to reverse theparin anticoagulation. One of the major components of salmine protamine is a 32 amino acid peptide having a total cationic charge of [+21], with carginine accounting for 67% of the total sequence and for all of the cost that charge is a 12 amino acid peptides of 20-40 amino acids with total cationic charge less than [+21] and which are able, at least partially, to reverse the effect of heparin and/or low molecular weight heparin anticoagulants are claimed, Specifically, the peptides are polycationic analogues of n-cramine where the positive charge on the amino acid sequence is reduced by selective replacement of positively charged arginine residues with an uncharged residue, so that total cationic charge is less than [+21]. The new peptides are used in vivo to reverse the effects of heparin; they have the same anti-heparin activity as protamine but are less toxic (because of the reduced number of positive charges) and are relatively
                                                                                                                                                                                                                                                                               Coagulation; anticoagulant; heparin; platelet aggregation; cell adhesion; positively charged cluster; arginine; polycationic; decrease; n-protamine; salmine protamine; protamine sulphate; salmon sperm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              charge of [+16] which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= repeat_region
/note= "4 tandem repeats of Ala(Lys)2(Ala)2(Lys)2 motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              easy and inexpensive to prepare. The present sequence represents a specific example of a protamine-like peptide with a charge of [+16] whi has been found to reverse the anticoagulation effects of both standard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide reversing the anticoagulant effects of heparin - is based on protamine but has fewer positive charges for reduced toxicity.
                                                                                                                                                                                                                                               Protamine-like peptide analogue P(AK2A2K2)4 with a charge of [+16].
                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "acetylated if C-terminus is amidated"
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27
                 ||| ||||| ||||| |||||| || :||||||| || akkaakkaak 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Andrews PC;
1 AKKYAKKAK--AEKAKKAYKAAEAKKAAK
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                                                                                                                                AAW06697 standard; peptide; 29
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/label= :
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                                                                                                                                                                                                                                                                                                                                                              Synthetic
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                                                                                           RESULT 13
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33.8%; 72.4%;

Query Match Best Local Similarity

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Gaps

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Length 29; 2; Indels

Score 72; DB 2; Pred. No. 0.46; 2; Mismatches

33.8%;

Best Local Similarity 72.4 Matches 21, Conservative

Query Match

Sequence 29 AA;

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The present sequence represents a synthetic peptide which has a high affinity for glycoaminoglycans and proteoglycans. The peptide is useful in methods for modulating heparin or other glycoaminoglycans with anticoagulant activity, promoting cell attachment or adhesion to natural or synthetic surfaces (especially vein grafts), modulating tumour cell entastasis, modulating cartilage differentiation, targeting drugs to epithelial cell surfaces (or to other cells expressing proteoglycans), modulating enzymes that act on glycoaminoglycan substrates, affinity purification of bioactive sequences of a glycoaminoglycan, modifying through glycoaminoglycans, and modulating wound healing. The peptide may also be used for blocking tissue uptake of heparin or other
                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel synthetic peptides with high affinity for glycoaminoglycans and proteoglycans, useful for modulating heparin, promoting cell attachment, modulating tumor metastasis and modulating wound healing.
                                                                                               Glycoaminoglycan; proteoglycan; heparin modulation; anticoagulant; cell attachment; cell adhesion; vein graft; tumour cell metastasis; cartilage differentiation; wound healing.
                                                                 Peptide modulating activity of heparin, and other glycans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure, Page 30; 76pp, English.
                                                                                                                                                                                                                                                                                                                                                                             San Antonio JD, Verrecchio A,
                                                                                                                                                                                                                                                                          02-FEB-2000; 2000WO-US002853.
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                                 (first entry)
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AAB08169;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel synthetic peptides with high affinity for glycoaminoglycans and proteoglycans, useful for modulating heparin, promoting cell attachment, modulating tumor metastasis and modulating wound healing.
   Gaps
                                                                                                                                                                                                                                                                                     Glycoaminoglycan; proteoglycan; heparin modulation; anticoagulant; cell attachment; cell adhesion; vein graft; tumour cell metastasis; cartilage differentiation; wound healing.
   4;
                                                                                                                                                                                                                                                         Peptide modulating activity of heparin, and other glycans.
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 Indels
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 Mismatches
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                                                     2 AKKAAKKAKKAAKKAKKA--AKKAKKAAK 28
                                   1 AKKYAKKAK--AEKAKKAYKAAEAKKAAK
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                                                                                                                                                    AAB08175 standard; peptide; 32 AA
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21; Conservative
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Schick BP;

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31.9%; Score 68; DB 3; Length 36; 58.3%; Pred. No. 1.6;
                           8; Indels
                                                        5 AKKAK-AEKAKKAYKAAEAKKAAKYEKA-AAEKAAA 38
                                                                        5; Mismatches
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ne: 158 secs
                            21; Conservative
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Gaps

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10; Indels

Pred. No. 1.1; 1; Mismatches

62.18;

Local Similarity

18;

Matches

Conservative

11 EKAKKAYKAAEAKKAAKYEKAAAEKAAAK 39

KKAAKAAAARKKAAKAAAAARKKAAK 31

AAB08169 standard; peptide; 36 AA.

RESULT 15 AABO8169 ID AABO XX

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June 3, 2005, 10:18:38 ; Search time 137 Seconds (without alignments) 113.544 Million cell updates/sec
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213
1 AKKYAKKAKAEKAKKAYKAA.....AKYEKAAAEKAAAKEAAYEA 45
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(cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
(cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
(cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
(cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
(cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
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(cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
(cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
(cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
(cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
(cgn2_6/ptodata/1/pubpaa/US106_PUBCOMB.pep:*
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(cgn2_6/ptodata/1/pubpaa/US108_NEW_PUB.pep:*
(cgn2_6/ptodata/1/pubpaa/US108_NEW_PUB.pep:*
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(cgn2_6/ptodata/1/pubpaa/US108_NEW_PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 45
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Perfect score:
Sequence:
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                                                                                                                                                                                                                                  Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 2, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 19, Appl	Sequence 5, Appli	Sequence 192079,	Sequence 200302,	Sequence 21, Appl	Sequence 26, Appl	Sequence 32, Appl	Sequence 33, Appl	Sequence 34, Appl
Ω1	US-09-816-989A-2	US-10-792-311-2	US-09-816-989A-1	US-10-792-311-1	US-10-667-004-19	US-10-219-626-5	US-10-437-963-192079	US-10-424-599-200302	US-10-667-004-21	US-10-667-004-26	US-09-805-301-32	US-09-805-301-33	US-09-805-301-34
DB	6	17	σ	17	16	14	16	15	16	16	6	6	δ
% Query Match Length DB	45	45	35	35	42	38	43	42	28	28	38	39	40
& Query Match	100.0	100.0	50.7	50.7	31.2	29.3	29.1	28.6	28.2	28.2	27.7	27.7	27.7
Score	213	213	108	108	66.5	62.5	62	61	9	09	59	59	59
Result No.	п	7	٣	4	'n	9	7	80	σ,	10	11	12	13

Sequence 35, Appl Sequence 36, Appl Sequence 37, Appl	Sequence 131, App Sequence 169296,	Sequence 38, Appl	Seguence 143465, Seguence 189981,	Sequence 6, Appli	71,	•	73,	129	Sequence 74, Appl	130	Sequence 75, Appl	Sequence 163175,	Sequence 222310,	Sequence 247483,	Sequence 45765, A	Sequence 128, App	Sequence 196023,	Sequence 262807,		71,		Sequence 151532,	Seguence 159371,	٠.	Sequence 143731,
9 US-09-805-301-35 9 US-09-805-301-36 9 US-09-805-301-37	9 US-09-805-301-131 15 US-10-424-599-169296 15 US-10-424-509-170053	9 US-09-805-301-38	15 US-10-424-599-143465 15 US-10-424-599-189981	14 US-10-219-626-6	9 US-09-805-301-71	9 US-09-805-301-72	9 US-09-805-301-73	9 US-09-805-301-129	9 US-09-805-301-74	9 US-09-805-301-130	9 US-09-805-301-75	15 US-10-424-599-163175	15 US-10-424-599-222310	15 US-10-424-599-247483	9 US-09-864-761-45765	9 US-09-805-301-128	15 US-10-424-599-196023	15 US-10-424-599-262807	US-1	0-490	15 US-10-324-143-119	-	15 US-10-424-599-159371	_	16 US-10-437-963-143731
.7 41 .7 42 .7 43			.7 45	.5 39	3. 39						.2 43		.2 44	.2 44		.8 40		4	4	26.5 25	~	c	٣	4	.3 45
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14 15 16	17 18	20	21 22	23	52 52	26	27	28	29	30	31	32	33	34	35	36	37	38	39			42	43	44	45

ALIGNMENTS

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APPLICANT: Gad, Alexander
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKE
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT APPLICATION NUMBER: 60/101,693
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR APPLICATION NUMBER: PCT/US99/22402
RRIOR APPLICATION NUMBER: PCT/US99/22402
RRIOR APPLICATION NUMBER: PCT/US99/22402
SPRIOR APPLICATION NUMBER: PCT/US99/22402
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 213; DB 9;
ilarity 100.0%; Pred. No. 3.5e-16;
Conservative 0; Mismatches 0;
              Sequence 2, Application US/09816989A
Patent No. US20020115103A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
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JS-09-816-989A-2
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Matches
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RESULT 2

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APPLICANT: Lis, Dories
TITLE OF INVENTION: COPOLYMENT I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKI
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKI
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/10/792,311
CURRENT APPLICATION NUMBER: US/09/816,989
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR PLING DATE: 2001-03-25
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR PLING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NOS: 7
TENEMED 1.
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APPLICANT: CHAN, Selena
APPLICANT: SU, Xing
APPLICANT: YAMAKAWA, Mineo
TITLE OF INVENTION: CONTROLLED ALIGNMENT OF NANO-BARCODES ENCODING SPECIFIC INFORMATIC
TITLE OF INVENTION: SCANNING PROBE MICROSCOPY (SPM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-10-792-311-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
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Best Local Similarity 64.4%; Pred. No. 5.6e-05;
Matches 29; Conservative 1; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: INTELIBIO-1(P14240X)
CURRENT APPLICATION NUMBER: US/10/667,004
CURRENT FILING DATE: 2003-09-19
FRIOR APPLICATION NUMBER: US 10/251,152
FRIOR FILING DATE: 2002-09-20
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PATENTIN VETSION 3.1
SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Synthetic peptide US-10-667-004-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19, Application US/10667004
Publication No. US20040126820A1
GENERAL INFORMATION:
Sequence 1, Application US/10792311
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial sequence
                        Publication No. US20050038233A1
GENERAL INFORMATION:
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US-10-667-004-19
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US-10-219-626-5
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                                                                                                   APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
APPLICANT: Gad, Doris
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REPERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/10/792,311
CURRENT FILING DATE: 2004-03-02
PRIOR RILING DATE: 2004-03-23
PRIOR FILING DATE: 1998-09-25
PRIOR PAPLICATION NUMBER: 60/101,693
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN Version 3.1
SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Gad, Alexander
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCTT-US
CURRENT PLING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAAYEA 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 213; DB 17;
Best Local Similarity 100.0%; Pred. No. 3.5e-16;
Matches 45; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09816989A Patent No. US20020115103A1
                     Sequence 2, Application US/10792311
Publication No. US20050038233A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -09-816-989A-1
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US-10-792-311-1
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APPLICANT: INTEL CORPORATION

APPLICANT: TWILL CORPORATION

APPLICANT: CHAN, Selena

APPLICANT: SU, Xing

APPLICANT: SCANNING PROBE MICROSCOPY (SPM)

FILE REFERENCE: INTELL310-1(P14240X)

CURRENT APPLICATION NUMBER: US/10/667,004

PRIOR APPLICATION NUMBER: US 10/251,152

PRIOR PLING DATE: 2002-09-20
                                                                                                                                                                                                     Sequence 200302, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: SOY Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223) B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 200302
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     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_2289C.1.pep
US-10-424-599-200302
17;
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                                                2 KKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEK 35
                                                                                       2 KKKKKKKKKKKKKKKKKKKKKKKKKKK 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 21, Application US/10667004
Publication No. US20040126820A1
GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.1
SEQ ID NO 21
LENGTH: 28
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Best Local Similarity 60.04
Matches 18; Conservative
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Matches 16; Conservative
     Conservative
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ORGANISM: Glycine max
     15;
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     Matches
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 192079
LENGTH: 43
TWOST
                                                                  APPLICANT: Phillips, Ross of APPLICANT: Phillips, Ross of APPLICANT: Phillips, Ross of APPLICANT: Phillips, Ross of APPLICANT: Welsh, John H
APPLICANT: Tratcher, David R
APPLICANT: Tryine, Alietair S
TITLE OF INVENTION: Compositions and Methods for Highly Efficient Transfection
FILE REFERENCE: CACO063
CURRENT APPLICATION NUMBER: US/10/219,626
CURRENT PILING DATE: 1998-02-12
PRIOR APPLICATION NUMBER: 09/022,614
PRIOR FILING DATE: 1998-02-12
PRIOR PLILING DATE: 1997-02-12
PRIOR PLILING DATE: 1997-02-12
PRIOR PLILING DATE: 1997-02-12
PRIOR APPLICATION NUMBER: 06/800,079
PRIOR PLILING DATE: 1997-02-12
PRIOR PLILING DATE: 1997-02-12
PRIOR PLILING DATE: 1997-02-12
PRIOR PLILING DATE: 1997-02-12
PRIOR FILING DATE: 1997-02-12
PRIOR FILING DATE: 1996-07-12
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US-10-437-963-192079
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Publication No. US20040123343A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 08/861,432
PRIOR FILING DATE: 1997-05-21
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.1
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Bucharov, Andrey A.
APPLICANT: Barbazuk, Brad
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44.1%;
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     Publication No. US20030100496A1
                                                   APPLICANT: Haines, Adrian M
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ORGANISM: Oryza sativa
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Best Local Similarity
Matches 19; Conserv
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Best Local Similarity
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1 Similarity 39.5%; Pred. No. 12;
15; Conservative 4; Mismatches 19; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MACROMOLECULE DELIVERY
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OPERATING SYSTEM: IBM P.C. DOS 6.0
SOFTWARE: WORD PARFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/805,301
FILING DATE: 12-Mar-2001
CLASSIPICATION: <unhalised columns of the co
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NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 217/189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
TOPOLGGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear; MOLECULE TYPE: peptide; SEQUENCE DESCRIPTION: SEQ ID NO: 32: US-09-805-301-32
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ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Silte 4700
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TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 33, Application US/09805301 Patent No. US20020173456A1 GENERAL INFORMATION:
                      TELEFAX: (213) 489-160
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 aming acids
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Hauer, Jochen
Mims, Martha P.
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LENGTH: 39 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 33:
                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
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STATE: California
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ZIP: 90071-2066
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Matches 15; Conserva
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APPLICANT: SOLUTION:
APPLICANT: SOLUTION: Solution
APPLICANT: SOLUTION: SOLUT
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Patent No. US20020173456A1
GENERAL INFORMATION:
APPLICANT: Smith, Louis C.
Sparrow, James T.
Hauer, Jochen
Mims, Martha P.
Mims, Martha P.
Mims, Martha P.
MITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 16;
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OPERATING SYSTEM: IBM P.C. DOS 6.0
SOFTWARE: WORD PERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/805,301
FILING DATE: 12-Mar-2001
CLASSIFFCATION: CHANOMD.>
PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
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NAME: Warburg, Richard J.
REGISTRATION WUMBER: 32,327
REFERENCE/DOCKET NUMBER: 217/189
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ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) OTHER INFORMATION: Synthetic peptide US-10-667-004-26
                                                                                                                   Sequence 26, Application US/10667004
Publication No. US20040126820A1
GENERAL INFORMATION:
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ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 60.04
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-805-301-32
                                                                                US-10-667-004-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
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27.7%; Score 59; DB 9; Length 41; 39.5%; Pred. No. 13;
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                                                           Sparrow, James T.
Hauer, Jochen
Mims, Martha P.
TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
MACROMOLECULE DELIVERY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MACROMOLECULE DELIVERY
                                                                                                                                                                                                                                                                                                                        ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 6.0
SOFTWARE: Word Perfect 6.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/805,301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFRENCE/DOCKET NUMBER: 217/189
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 35:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/584,043
                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 36, Application US/09805301; Patent No. US20020173456A1; Patent No. US20020173456A1; APPLICANT: Smith, Louis C.; Hauer, Jochen; Hauer, Martha P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 12-Mar-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                      APPLICANT: Smith, Louis C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 35:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                NUMBER OF SEQUENCES: 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                               CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15; Conservative
Patent No. US20020173456A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
US-09-805-301-36
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                     Length 39;
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                                                             4; Mismatches 19; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 KKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAK 39
                                                                                                                                         2 KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK 39
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                                                                                                                                                                                                                                                                                                                                                            Mims, Martha P.
TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
MACROMOLECULE DELIVERY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 59; DB 9;
Pred. No. 12;
4; Mismatches 15
                       Score 59; DB 9;
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 6.0
SOFTWARE: WORD Perfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/805,301
FILING DATE: 12-Mar-2001
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/584,043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 217/189
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-09-805-301-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 27.7%; Score 59;
Best Local Similarity 39.5%; Pred. No. 3
Matches 15; Conservative 4; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                        Sequence 34, Application US/09805301
Patent No. US20020173456A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 35, Application US/09805301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 34:
                                                                                                                                                                                                                                                                                                     APPLICANT: Smith, Louis C. Sparrow, James T. Hauer, Jochen Mims, Martha P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 40 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              storage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                   27.7%;
illarity 39.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                Query Match
Best Local Similarity
Matches 15; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
US-09-805-301-35
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Indels

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CITY: LOB Angeles
STARE: California
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MD
STORAGE
COMPUTER READABLE FORM:
BECASAGE
COMPUTER: 13.5" Diskette, 1.44 MD
STORAGE
COMPUTER: 13.5" Diskette, 1.44 MD
STORAGE: Word Perfect 6.1
CURRENT APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/09/805,301
FILING DATE: 12-Mar-2001
FILING DATE: 12-Mar-2001
FILING DATE: 12-Mar-2001
FILING DATE: UDKNOWN:
APPLICATION NUMBER: 08/584,043
ATTORNEY/AGENT INFORMATION:
MAME: Warburg, Richard J.
REGISTRATION NUMBER: 217/189
TELECOMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
TELERACTHORICATION: GIAS
TELERACTHORICATION: GIAS
TYPE: amino acid
STRANDENSES: SINGLE
TYPE: amino acid
STRANDENSES: SINGLE
TYPE: amino acid
STRANDENSES: SINGLE
TOPOLOGY: linear
MOLECULE TYPE: peptide

105-09-805-301-36
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0; Gaps

Query Match 27.7%; Score 59; DB 9; Length 427-Best Local Similarity 39.5%; Pred. No. 13; Matches 15; Conservative 4; Mismatches 19; Indels

2 KKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAK 39

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Search completed: June 3, 2005, 10:31:26 Job time : 138 secs us-10-792-311-2.rai

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US-09-405-743A-2
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US-09-816-989A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
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                                                                                                                                                                                    3, 2005, 10:11:57; Search time 42 Seconds (without alignments) 79.981 Million cell updates/sec
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Sequence 13, 3
Sequence 15, 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
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Sequence
Sequence
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Sequence
Sequence
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Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cgm2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgm2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgm2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgm2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgm2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgm2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-405-743A-2
US-09-816-989A-1
US-09-816-989A-1
US-08-152-488-13
US-08-677-304-13
US-08-677-304-13
US-08-436-703B-2
US-08-436-703B-4
US-08-436-703B-4
US-08-136-488-10
US-08-136-488-11
US-08-136-11
US-08-136-11
US-08-303-025-13
US-08-436-703B-3
US-08-436-703B-3
US-08-436-703B-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                   - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query
Match Length DB
                                                                                                                                                                                                                                                                                                                           US-10-792-311-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0 Maximum DB seq length: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
                                                                                                                                OM protein
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database
                                                                                                                                                                                              Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Result
No.
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Sequence 2, Application US/09816989A

Fatent No. 6800287

GENERAL INFORMATION:
APPLICANT: Lis, Doris

TILLE OF INVENTION:
FILE REFERENCE: 2609/60807-A-PCT-US

CURRENT APPLICATION NUMBER: US/09/816,989A

CURRENT FILING DATE: 2001-03-23

PRIOR PILING DATE: 1999-09-25

FRICE APPLICATION NUMBER: PCI/US99/22402

PRIOR FILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 7

SOFTWARE PLANCE DATE: 1999-09-24

SEQ ID NO 2

LENGTH: 45
                                                                                                       ,8', App.
58, Appl
ace 32, Appl
ace 2, Appl
yence 32, Appl
yence 32, Appl
Sequence 34, Appl
Sequence 35, Appl
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               Sequence
Sequence
Sequence
Sequence
Sequence
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US-09-405-743A-2
                                                                          Sequence
                                                                                                 Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09405743A

Patent No. 6514338
GENERAL INFORMATION:
APPLICANT: Yeds Research and Development Co., Ltd.
APPLICANT: Yeds Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT APPLICATION NUMBER: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 213; DB 4; Similarity 100.0%; Pred. No. 1.9e-16;
US-09-344-529-5
US-08-839-624-25
US-09-150-812-25
US-09-221-050-10
US-09-247-054-14
US-08-995-172-21
US-08-960-890A-58
US-08-460-890A-58
US-08-167-641C-58
US-08-167-641C-58
US-08-117-121-32
US-09-117-121-35
US-09-221-050-2
US-08-584-043A-33
US-08-584-043A-33
US-08-584-043A-33
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                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
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5

Gaps

10;

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Query Match 35.0%; Score 74.5; DB 1; Length 32; Best Local Similarity 68.8%; Pred. No. 0.081; Matches 22; Conservative 3; Mismatches 4; Indels
5; Indels
                                              1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAAYEA 45
                                                                                        --- KEAKAKAAEAAKEAAYEA 35
                                                                                                                                                                                                                                                                                                                                                           FOR HEPARIN AND
                                                                                                                                                                                             ; Sequence 13, Application US/08152488
; Patent No. 5534619
; GENERAL INFORMATION:
APPLICANT: Wakefield, Thomas W.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN
TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
TITLE OF INVENTION: ANTICOAGULATION REVERSAL
COMMER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: WordPerfect 6; ASCII (DOS) Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/152,488
FILING DATE: 12-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 AKKA-AKKAKKA-AKKAKKAAKKAAKKA 30
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
ATTORNEY AGENT INFORMATION:
NAME: Rohm, Benita J.
REGISTRATION NUMBER: 28,664
REFERENCE/DOCKET NUMBER: RM-7WG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-276-3344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New Jersey
: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE: N/A
PUBLICATION INFORMATION:
DOCUMENT NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
US-08-152-488-13
                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: New 7-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 07016-1811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
                                                                                             1 AKKYAKKEKA--AKKAYK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . TELEFAX: 908-276-5543
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: N/A PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS: ADDRESSE: Benita J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: N/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: N/A MOLECULE TYPE: POORIGINAL SOURCE:
                                                                                                                                                                RESULT 5
US-08-152-488-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-303-025-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS:
  Matches
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lis, Doris
APPLICANT: Lis, Doris
APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: CAPOLY-OS
TITLE OF INVENTION WUMBER: US/09/816,989A
CURRENT APPLICATION NUMBER: 60/101,693
PRIOR FILING DATE: 1998-09-25
PRIOR PILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PARCHIN VERSION 3.1
SEQ ID NO 1
LENGTH: 35
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                   ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-9898-2
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Sequence 1, Application US/09405743A
GENERAL INFORMATION:
APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
CURRENT APPLICATION UNDER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
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                                                                                                                                         ; Score 213; DB 4; Length 45;
; Pred. No. 1.9e-16;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 50.7%; Score 108; DB 4; Length 35; Best Local Similarity 64.4%; Pred. No. 2.4e-05; Matches 29; Conservative 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.7%; Score 108; DB 4; Length 35; 64.4%; Pred. No. 2.4e-05;
                                                                                                                                                                                                                                                                  1 AKKYAKKAKABEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAAYEA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AKKYAKKEKA--AKKAYK-----KEAKAKAAEAAKEAAYEA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAAYEA 45
                                                                                                                                                                                                                                     1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAAYEA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09816989A Patent No. 6800287
                                                                                                                                         Query Match
Best Local Similarity 100.0%;
Matches 45; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                              JS-09-405-743A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-405-743A-1
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LENGTH: 35
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; Patent No. 5919761
; GENERAL INFORMATION:
    APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
    APPLICANT: Stanley, James C.
    TITLE OF INVENTION: NOVEL PEPTIDES FOR TITLE OF INVENTION: WEIGHT HEPARIN AND LOW MOLECULAR; TITLE OF INVENTION: WEIGHT HEPARIN REVERSAL; TITLE OF INVENTION: ANTICOAGULATION REVERSAL; NUMBER OF SEQUENCES: 18
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Benita J, Rohm, Esq.
                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6; ASCII (DOS) Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/677,304
FILING DATE:
CLASSIPICATION: 530
PRIOR APPLICATION NUMBER: US/08/152,488
FILING DATE: 12-NOV-1993
APPLICATION NUMBER: US/08/152,488
FILING DATE: 12-NOV-1993
APPLICATION NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
APPLICATION NUMBER: 28,664
REFERENCE/DOCKET NUMBER: 28,664
REFERENCE/DOCKET NUMBER: 28,664
REFERENCE/DOCKET NUMBER: CA: 3844
TELEFRAN: 908-276-5543
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH 32 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: ADDECTION TYPE: PEPTING
TOPOLOGY: NO: 5771212 Relevant
MOLECULE TYPE: PEPTING:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 AKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKA 36
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                                                                                                                   CITY: Cranford
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07016-1811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE: N/A
PUBLICATION INFORMATION:
DOCUMENT NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
US-08-677-304-13
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STREET: 6601 Woodward Avenue
STREET: Suite 1525
CITY: Detroit
                          CORRESPONDENCE ADDRESS:
ADDRESSER: Benita J. Rohm, Esq. STREET: 512 Springfield Avenue CITY: Cranford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 35.09
Best Local Similarity 68.89
Matches 22, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
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0.081;
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Patent No. 5721212
GENERAL INFORMATION:
APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEBARIN AND TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEBARIN TITLE OF INVENTION: ANTICOAGULATION REVERSAL
                                                                                   APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: NOVEL PECTIDES FOR HEPARIN AND TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN TITLE OF INVENTION: ANTICOAGULATION REVERSAL
                                                                                                                                                                                                                                                                                                                                                                                           STATE: Michigan

COUNTRY: United States of America

ZIF: 48256-4415

COMPUTER: EADABLE FORM:

MEDIUM TYPE: Floppy diskette 3.5" 1.44Mb

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING STATE: MS-DOS V.6.22

SOFTWARE: WORDPERFECT 6.1; ASCII (DOS)Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/303,025

FILING DATE: 08-SEFT-1994

CLASSIPICATION BATA:

APPLICATION NUMBER: PCT/US92/06829

FILING DATE: 14-AUG-1992

APPLICATION NUMBER: US 08/152,488

FILING DATE: 12-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: Rohm, Benita J.

REFERENCE/DOCKET NUMBER: 7WH-060548-00231

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 AKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKA 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 35.0%; Score 74.5; D
Best Local Similarity 68.8%; Pred. No. 0.08
Matches 22; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Benita J, Rohm, Esq.
STREET: 150 West Jefferson, Suite 2500
CITY: Detroit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; DOCUMENT NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993
US-08-303-025-15
Sequence 15, Application US/08303025
Patent No. 5614494
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: N/A
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: N/A
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: N/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N/A
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Score 74.5; DB 1; Length 33;
Pred. No. 0.083;
3; Mismatches 4; Indels
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APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
APPLICANT: Andrews, Philip C.
APPLICANT: Andrews, Philip C.
APPLICANT: Attaches, James C.
TITLE OF INVENTION: HEPARIN AND LOW MOLECULAR
TITLE OF INVENTION: WEIGHT HEPARIN
TITLE OF INVENTION: ANTICOAGULATION REVERSAL
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE Benita J, Rohm, Esq.
STREET: 6601 Woodward Avenue
                 PRICE APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06829
FILING DATE: 14-AUG-1992
APPLICATION NUMBER: US 08/152,488
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rohn, Benita J.
REFERENCE/DOCKET NUMBER: 7WH-060548-00231
TELEPHONE: 313-496-7622
TELEPHONE: 313-496-7622
TELEPAX: 313-496-7622
TELEPAX: 313-496-7622
TELEPAX: 313-496-7622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 AKKA-AKKAKKA-AKKAKKAKKAKKAKKA 31
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SOFTWARE: ASCII (DOS) Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,703B
FILING DATE: 08-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Rloppy disk 1.44Mb, 3.5"
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Detroit
STATE: Michigan
COUNTRY: United States of America
ZIP: 48226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE: N/A

DOCUMENT NUMBER: PCT/US92/08069

FILING DATE: 14-AUG-1993

US-08-303-025-16
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Patent No. 5919761
GENERAL INFORMATION:
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Best Local Similarity 68.8%;
Matches 22; Conservative
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ATTORNEY/AGENT INFORMATION:
NAME: Rohm, Benita J.
                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                            peptide
                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: N/A MOLECULE TYPE: po ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JS-08-436-703B-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16, Application US/0830325
Patent No. 5614494
GENERAL INFORMATION:
APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN TITLE OF INVENTION: ANTICOAGULATION REVERSAL
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEB: Benita J, Rohm, Esq.
STREET: 150 West Jefferson, Suite 2500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy diskette 3.5" 1.44Mb COMPUTER: IBM PC COMPALIALE COMPUTED: DERATING SYSTEM: MS-DOS v.6.22 SOFTWARE: WordPerfect 6.1; ASCII (DOS) Text CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/303,025 FILING DATE: 08-SEPT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 AKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKA 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       7WK-060548-00233
                                                          COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk 1.44Mb, 3.5"
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS_DOS
SOFTWARE: MOTCHERECT 6;
SOFTWARE: ASCII (DOS) Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,703B
FILING DATE: 08-MAY-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: N/A
FILING DATE: N/A
ATTORNEY/AGENT INFORMATION:
NAME: ROHM, BENTEAL 3,
REGISTRATION NUMBER: 28,664
REGISTRATION NUMBER: 28,664
REGISTRATION NUMBER: 28,664
: Michigan
XY: United States of America
48226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Michigan
COUNTRY: United States of America
ZIP: 48226-4415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 313-965-1976
TELEPHONE: 313-965-1951
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 68.8
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: N/A
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Detroit
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US-08-436-703B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-303-025-16
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Gaps

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Madrews, Philip C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN TITLE OF INVENTION: ANTICOAGULATION REVERSAL NUMBER OF SEQUENCES:
TITLE OF SEQUENCES:
TORRESPONDENCE ADDRESS:
ADDRESSEE: Benita J, Rohm, Esq.
STREET: 512 Springfield Avenue
CITY: Cranford
STREET: 512 Springfield Avenue
CITY: Cranford
STREET: 512 Springfield Avenue
CITY: Cranford
STREET: 151 Springfield Avenue
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CITY: Cranford
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CITY: Cranford
STREET: 151 Springfield Avenue
STREET: 1
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         ) ORIGINAL SOURCE:
CREANISM: N/A
HULLCATION INFORMATION:
AUTHORS: N/A
HILLE: N/A
PUBLICATION INFORMATION:
DOCUMENT NUMBER: PCT/US92/08069
HILLO BATE: 14-AUG-1993
US-08-152-488-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOCUMENT NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993
US-08-152-488-11
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-276-3344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11, Application US/08152488 Patent No. 5534619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPAX: 908-276-5545
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
ORIGINAL SOURCE:
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Sequence 10, Application US/08152488

Factor No. 5534619

GENERAL INFORMATION:

APPLICANT: Wakefield, Thomas W.

APPLICANT: Andrews, Philip C.

APPLICANT: Stanley, James C.

TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN TITLE OF INVENTION: ANTICOAGULATION REVERSAL NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Benita J, Rohm, Esq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONDESCEE: Benita J, Rohm, Esq.
STREET: 512 Springfield Avenue
CITY: Cranford
STATE: New Jersey
COUNTRY: United States of America
ZIP: 0710f-1811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DGS
SOFTWARE: MORDER: US-DGS
SOFTWARE: WORDPER: US-DGS
SOFTWARE: WORDPER: US-DGS
SOFTWARE: 12-NOV-1993
FLING DATE: 12-NOV-1993
FLING DATE: 14-AUG-1993
ATTORNEY, AGENT INFORMATION:
NAME: ROHM, Benita J.
NAME: NOW OFF-SE-J344
TELEPHONE: 908-276-3344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 AKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 AKKA-AKKAKKA-AKKAKKAAKKAAKKA 31
                                               7WK-060548-00233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
REGISTRATION NUMBER: 28,664
REFERENCE/DOCKET NUMBER: 7WK-(
TELECOMUNICATION INFORMATION:
TELEPHONE: 313-965-1976
TELEFAX: 313-965-1951
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
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INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 68.8
Matches 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
                                                                                                                                                                                                                                                                                  STRANDEDNESS: N/A
TOPOLOGY: N/A
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
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STRANDEDNESS: N/A
TOPOLOGY: N/A
                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TITLE: N/A
US-08-436-703B-4
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33.8%; Score 72; DB 1; Length 29; 72.4%; Pred. No. 0.14;
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                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: NOWEL PEPTIDES FOR HEPARIN AND
TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
TITLE OF INVENTION: LOW MOLECULAR WEIGHT ESON
TITLE OF INVENTION WINGER: LOW COMPUTER: MACHORITE FORM: MS-DOS v.6.22
SOFTWARE: WORTHER FORM: MS-DOS v.6.22
SOFTWARE: WORTHER HEADALCATION DATA:
APPLICATION NUMBER: US/08/303,025
FILING DATE: 14-AUG-1994
CLLASSIFICATION NUMBER: US/08/152,488
FILING DATE: 14-AUG-1993
ATTORNER APPLICATION NUMBER: US/08/152,488
FILING DATE: 12-NOV-1993
ATTORNER MORE NOW SHAFT INFORMATION:
NAME: REPERRENCE/DOCKET NUMBER: THEORY MENTER INFORMATION:
NAME: REPERRENCE/DOCKET NUMBER: THEORY MENTER INFORMATION:
NAME: REPERRENCE/DOCKET NUMBER: THEORY MENTER INFORMATION:
NAME: ROADSITUATION WINDER: NOW MENTER INFORMATION:
NAME: ROADSITUATION WINDER: NOW MENTER INFORMATION:
NAME: ROADSITUATION WINDER: NOW MENTER INFORMATION:
NAME: ROADSITUATION WINDER: NAME: NAME: ROADSITUATION WINDER: NAME: N
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DOCUMENT NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred.
                                                            Sequence 11, Application US/08303025
Patent No. 5614494
GENERAL INFORMATION:
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Patent No. 561494
GENERAL INFORMATION:
APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 313-496-7622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 313-496-8454
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 29 amino acids
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PUBLICATION INFORMATION:
AUTHORS: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
TOPOLOGY: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
US-08-303-025-13
                                         US-08-303-025-11
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                                                                      Gaps
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Query Match 33.8%; Score 72; DB 1; Length 29; Best Local Similarity 72.4%; Pred. No. 0.14; Matches 21; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                              Patent No. 564494
GENERAL INFORMATION:
APPLICANT: Wakefield, Thomas W.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND TITLE OF INVENTION: ANTICOAGULATION REVERSAL NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benita J, Rohm, Esq.
STREET: 150 West Jefferson, Suite 2500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy diskette 3.5" 1.44Mb
COMPUTER: Thoppy diskette 3.5" 1.44Mb
COMPUTER: Thoppy diskette 3.5" 1.44Mb
COMPUTER: Thoppy diskette 3.5" 1.44Mb
COMPUTER: The PC compatible
OPERATING SYSTEM: MS-DOS v.6.22
SOFTWARE: WordPerfect 6.1; ASCII (DOS) Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,025
FILING DATE: 0.8-SEPT-1994
CLASSIPICATION NUMBER: PCT/US92/06829
FILING DATE: 14-AUG-1992
APPLICATION NUMBER: US 08/152,488
FILING DATE: 11-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: ROAM, BENILA J.
REFERENCE DOCKET NUMBER: 7WH-060548-00231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 AKKAAKKAAKKAKAA--AKKAKKAAK 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AKKYAKKAK--AEKAKKAYKAAEAKKAAK 27
                                                                                                                               1 AKKYAKKAK--AEKAKKAYKAAEAKKAAK 27
                                                                                                                                                               2 AKKAAKKAAKKAA-AKKAKA 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Michigan
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; DOCUMENT NUMBER: PCT/US92/08069
; FILING DATE: 14-AUG-1993
US-08-303-025-10
                                                                                                                                                                                                                                                                                                       US-08-303-025-10
; Sequence 10, Application US/08303025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 313-496-7622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 313-496-8454
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: N/A
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: N/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Detroit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Simi
Matches 21;
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Query Match 33.8%; Score 72; DB 1; Length 29; Best Local Similarity 72.4%; Pred. No. 0.14; Matches 21; Conservative 2; Mismatches 2; Indels
TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS: 16
CORRESPONDENCE ADDRESS: 16
CORRESPONDENCE ADDRESS: 16
STREET: 150 Weet Jefferson, Suite 2500
CITY: Detroit and 1826-441
STRYE: Michigan
COUNTRY: United States of America 2TP: 48226-441
COMPUTER: BADABLE FORM: MS-DOS v.6.22
SOFTWARE: Michigan COMPATA: PRADABLE FORM: MS-DOS v.6.22
SOFTWARE: MICHIGANION DATA: APPLICATION DATA: 4806/303,025
FILING DATE: 14-AUG-1992
APPLICATION NUMBER: US 08/152,488
FILING DATE: 12-NOV-1993
ATTOMEY AGENTIAN NUMBER: PCT/US92/06829
FILING DATE: 12-NOV-1993
ATTOMEY ACKET INFORMATION: MARE: Rohm Benita J. 1846-7622
TELEFRANE: MICHIGA DATE: 12-NOV-1993
ATTOMEY ACKET NUMBER: TAH-060548-00231
TELEFRANE: 1313-496-7622
INFORMATION POR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS: LEMCTH ADDRESS: N/A
TOPOLOGY: N/A
MOLECULE TYPE: apping acids STRANDEDNESS: N/A
TILING DATE: 11-NOW-1993
ATTOMEY ACT STRONG ACID NO: 13: SEQUENCE CHARACTERISTICS: CHARACTE
                                  NOVEL PEPTIDES: FOR HEPARIN AND
LOW MOLECULAR WEIGHT HEPARIN
ANTICOAGULATION REVERSAL
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1 AKKYAKKAK--AEKAKKAYKAAEAKKAAK 27 2 AKKAAKKAKKAKKA--AKKAKKAAK 28 ð

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4; Gaps

Search completed: June 3, 2005, 10:19:59 Job time: 43 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

June 3, 2005, 10:28:13 ; Search time 38 Seconds (without alignments)
141.793 Million cell updates/sec

Title: Perfect score: Sequence:

US-10-792-311-3 266 1 AKKYAKKEKAYAKKAEKAAK......BAKYKABAAKAAAKEA 56

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

14225 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 56

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

CITMMADIEC

	Description		protamine phi-3.3		antifreeze protein	tandem repeat pept	ribosomal protein	antifreeze protein	myosin catalytic l		probable motility	probable histone H	homeotic protein u	histone H3.2 - Tet	protamine S4 - sma	hypothetical prote	ribosomal protein	antifreeze protein	conserved hypothet	antifreeze protein	hypothetical prote	hypothetical prote	5	hypothetical prote	tropomyosin - huma	Sry-related sequen	neurofilament trip	Sry-related sequen		hypothetical prote
SUMMARIES	σı	804941	S10545	S10544	A05163	PT0028	S78292	FDF18G	S01945	A56371	P71847	T07842	S58853	S10263	A41270	T07242	S20835	FDFISG	AC0896	FDFL3W	D69950	H83869	B83145	AE0612	165746	I50193	802571	150190	F69800	A82865
	DB	7	~	7	~	~	~	ч	~	~	2	~	~	N	~	~	~	н	~	-	~	~	~	~	~	7	~	~	7	7
	Query Match Length	45	45	45	45	44	54	40	52	51	54	26	40	41	32	49	55	33	54	37	46	47	20	35	42	54	30	54	36	44
*	Query	25.8	24.8	24.2	22.9	21.6	21.6	21.1	20.1	19.9	19.9	19.2	18.8	17.3	16.7	16.7	16.5	16.4	16.4	16.2	16.0	16.0	16.0	15.8	'n.		15.6		15.4	15.4
	Score	68.5	99	64.5	61	57.5	57.5	26	53.5	53	53	51	20	46	44.5	44.5	44	43.5	43.5	43	42.5	42.5	42.5	42	42	42	41.5	41.5	41	41
	Result No.		7	m	4	Ω.	9	7	8	ტ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

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Gaps 8;

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Query Match 24.8%; Score 66; DB 2; Length 45; Best Local Similarity 41.2%; Pred. No. 16; Matches 21; Conservative 6; Mismatches 16; Indels

probable ribosomal Sry-related sequen	antifreeze protein chromogranin-B - r hypothetical prote	p83/100 protein - histone H1 - sea u	hypothetical prote duplicated hypothe	hypothetical prote Sry-related sequen probable periplasm	conserved hypothet hypothetical prote repa protein - Lac
C72528 I50027	A05162 F49164 E70227	S61469 PL0069	H2/5/8 B87570 F81886	F81135 I50191 G81434	E87173 S56691 S15953
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50	33 26 47	8 T C	532	5 5 4 5 4 5	50 23
15.4	15.2	15.0	15.0	15.0	15.0 14.8 14.8
41	40.5 40 40	444	444	4 4 4 0 0 0	39.5 39.5
30 31	3 3 5 4 3 5	365	3 8 6 3 8 8 7	4 4 4 0 1 2	444

ALIGNMENTS

RESULT 1 \$04941 protamine phi-3.1 - California mussel protamine phi-3.1 - California mussel N;Alternate names: protamine PL-IV.1 C;Species: Mytilus californianus (California mussel) C;Accession: S04941 C;Accession: S04941 R;Ausio, J.; McParland, R. Eur., U. Biochem. 182, 569-576, 1989 A;Title: Sequence and characterization of the sperm-specific protein phi3 from Mytilus can also and characterization of the sperm-specific protein phi3 from Mytilus can also south and can also and characterization of the sperm-specific protein phi3 from Mytilus can also south and

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A,Cross-references: UNIPROT:P11860 C,Superfamily: histone H1 C,Keywords: DNA binding; nucleus

A; Molecule type: protein A; Residues: 1-45 < AUS> A; Accession: S10544

Local Similarity 39.29 tes 20, Conservative

Best Loca Matches

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Query Match

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C;Accession: S07046
R;Chakrabartty, A: Hew, C.L.; Shears, M.; Pletcher, G.
Can. J. Zool. 66, 403-408, 1988
A;Title: Primary structures of the alanine-rich antifreeze polypeptides from grubby scult A;Reference number: S06417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Odontella sinensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-54 «KON»
A; Cross-references: EMBL: 667753; NID: 91185127; PIDN: CAA91665.1; PID: 91185182
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           myosin catalytic light chain, ventricular and slow striated muscle - mouse (fragment)
                                                                                   2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: S78292
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                ribosomal protein L32', chloroplast - Odontella sinensis chloroplast
C;Species: chloroplast Odontella sinensis
C;Date: 17-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 20-Jun-2000
C;Accession: S78292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antifreeze protein GS-8 - grubby sculpin
C;Species: Myoxocephalus aenaeus (grubby sculpin)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Kowallik, K.V.; Stoebe, B.; Schaffran, I.; Kroth-Pancic, P.; Freier, Plant Mol. Biol. Rep. 13, 336-342, 1995
A;Title: The Chloroplast Genome of a chlorophyll a+c- containing Alga,
                                      Length 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Cross-references: UNIPROT:P20617
C,Superfamily: antifreeze protein
C,Keywords: antifreeze; blocked amino end
F;I/Modified site: blocked amino end (Met) #status experimental
                                                                                                                                                                                  Indels
                                                                                                                                                 14 KAEKAAKKAEAKAYKAAEAKKKAE--AKYKAEAAKAAAKEAAYE 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Gene: rp132,
A,Genome: chloroplast
C,Superfamily: rice chloroplast ribosomal protein L32
C,Keywords: chloroplast; protein biosynthesis; ribosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11,
                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAK 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 57.5; DB Fred. No. 92; 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 AEKAAKKAEAKAYKAAEAKKKAEAKYKAEAAKAA
                             21.6%; Score 57.5; D
40.9%; Pred. No. 79;
:ive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
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Pred. No. 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N'Alternate names: myosin alkali light chain
C;Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21.6%;
45.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21.1%;
                                                                                         18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 45.5
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: S78238
                             Query Match
Best Local Similarity
Matches 18; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Accession: S07046
A:Molecule type: protein
A;Residues: 1-40 <CHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 17; Conserv
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C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: P7028
R;Wallis, A.E.; McMaster, W.R.
J. Exp. Med. 166, 1814-1824, 1987
A;Title: Identification of Leishmania genes encoding proteins containing tandemly repeat
A;Reference number: P70027; MUID:88061089; PMID:3502718
                                                                                                                                  protamine phi-3.2 - California mussel
NiAlternate names: protamine PL-IV.2
C;Species: Mytilus californianus (California mussel)
C;Decies: Mytilus californianus (California mussel)
C;Dete: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: S10544
C;Accession: S10544
Bur. J: MCParland, R.
Bur. J: MoParland, R.
Bur. J: Blochem. 182, 569-576, 1989
A;Title: Sequence and characterization of the sperm-specific protein phi3 from Mytilus
A;Reference number: S04941; MUID:89325302; PMID:2666130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antifreeze protein SS-8 - shorthorn sculpin
C;Species: Myoxocephalus scorpius (shorthorn sculpin, daddy sculpin)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: Mo5163
R; Hew, C.L.; Joshi, S.; Wang, N.C.; Kao, M.H.; Ananthanarayanan, V.S. Bur. J. Biochem. 151, 167-172, 1985
A; Title: Structures of shorthorn sculpin antifreeze polypeptides. A; Mccession: A05163
A; Mccession: A05163
A; Molecule type: protein
A; Mcseidues: 1-45 < HEW>
AKRSPRKKKAAVKKSSK----SKAKKPKSPKKKKAA--KKPARKAAKKK 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKYKAEAAKAAKE 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tandem repeat peptide chain - Leishmania major (clone 39) (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.2%; Score 64.5; DB 2; Length 45; 39.2%; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;1/Modified site: blocked amino end (Met) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 22.9%; Score 61; DB 2; Length 45; Best Local Similarity 47.4%; Pred. No. 41; Matches 18; Conservative 4; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 AKKAEKAAKKAEAKAYKAAEAKKKAEAKYKAEAAKAAA 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15;
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C;Superfamily: antifreeze protein
C;Keywords: antifreeze; blocked amino end; plasma
F;9-45/Region: alanine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Accession: PT0028
A; Molecule type: mRNA
A; Residues: 1-44 <WAS>
A; Cross-references: UNIPROT:P14700; EMBL:X06556
A; Experimental source: strain NIH S
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Query Match

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A;Cross-references: UNIPROT:049175; EMBL:AF042182; NID:g2809203; PIDN:AAB97684.1; PID:g28
A;Experimental source: cv. oleifera
C;Function:
A;Description: histone H3 plays a key role in nucleosome formation
C;Keywords: DNA binding; nucleosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  function in flies and butterflies.
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A; Cross-references: UNIPROT: Q25210; EMBL: L42137
A; Arote: the nucleotide sequence was submitted to the EMBL Data Library, May 1995
C; Superfamily: homeobox homology
C; Keywords: DNA binding; homeobox; nucleus; transcription regulation
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NyAlternate names: ultrabithorax homeodomain protein
Cippecies: Junonia coenia
Cippecies: Junonia coenia
Cipate: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 16-Aug-2004
Cipate: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 16-Aug-2004
Cipate: 19-Mar-1997
RyMarren, R.W.; Nagy, L.; Selegue, J.; Gates, J.; Carroll, S.
Nature 372, 458-461, 1994
Ayritle: Bvolution of homeotic gene regulation and function in flies and but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S10263
histone H3.2 - Tetrahymena borealis (fragment)
histone H3.2 - Tetrahymena borealis (fragment)
C;Species: Tetrahymena borealis
C;Species: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C;Accession: S10263
C;Accession: S10263
R;Brunk, C.F.; Kahn, R.W.; Sadler, L.A.
J. Mol. Evol. 30, 290-297, 1990
                                                                                                                                                                                                                                                                                                         probable histone H1-3 - rape (fragment)
C;Species: Brassica napus (rape)
C;Species: Tay-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
C;Accession: T07842.
R;Deleu, C.; Coustaut, M.; Niogret, M.P.; Larher, F.
submitted to the EMBL Data Library, January 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 40;
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                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                th 18.8%; Score 50; DB 2; Le Similarity 40.0%; Pred. No. 3.1e+02; 14; Conservative 4; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 19.2%; Score 51; DB 2; I
Local Similarity 35.1%; Pred. No. 3.3e+02;
Nes 13; Conservative 5; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 KAEAKAYKAAEAKKKAEAKYKAEAAKAAAKEAAYE 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Accession: T07842
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1-56 <DEL>
                                                                                                                                                       19 AYAHKDKKDAKKPELSSQLVAHKDKKDAKKPKNSVA
                                                                                           10 AYAKKAEKAAKKAEAKAYKAAEAKKKAEAKYKAEAA
41.78;
Best Local Similarity 41.7
Matches 15; Conservative
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C;Species: Helicobacter pylori
A;Variety: strain J99
A;Variety: strain J99
A;Variety: strain J99
A;Variety: L: Eab-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: F71847
B;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, B.D.; Doig, P.C.; Smith, D.R.;
Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.B.; Vovis, G.F.;
Inter C; C; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.B.; Vovis, G.F.;
A;Tile: Genomic sequence comparison of two unrelated isolates of the human gastric path
A;Reference number: A71800; MUID:99120557; PMID:9923682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R,Zhidkova, N.I.; Justice, S.K.; Mayne, R.
J. Biol. Chem. 270, 9486-9493, 1995
A;Title: Alternative mRNA processing occurs in the variable region of the pro-alpha 1(XI
A;Reference number: A56371; MUID:95238468; PMID:7721876
      C; Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C; Accession: S01945
R; Cohen, A.; Barton, P.J.R.; Robert, B.; Garner, I.; Alonso, S.; Buckingham, M.E.
Nucleic Acidos Res. 16, 10037-10052, 1988
A; Title: Promoter analysis of myosin alkali light chain genes expressed in mouse striate
A; Reference number: S01944, MUID:89057447; PMID:3194193
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A;Experimental source: strain J99
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C;Species: Homo sapiens (man)
C;Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 15-Sep-2003
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                                                                                                                                                                                                                                                                                                                                                                                                    Length 52;
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                                                                                                                                                                                       A,Accession: S01945
A;Molecule type: DNA
A;Residues: 1-52 <COHA
A;Cross-references: UNIPROT:P09542; EMBL:X12972
C;Superfamily: calmodulin; calmodulin repeat homology
C;Keywords: EF hand; muscle
                                                                                                                                                                                                                                                                                                                                                                                                 Score 53.5; DB 2;
Pred. No. 1.9e+02;
3; Mismatches 15;
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A;Molecule type: DNA
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A;Map position: 1p21-1p21
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Local Similarity 42.0%;
nes 21; Conservative 3
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hes 13; Conservative
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A,Molecule type: DNA
A,Residues: 1-54 <ARN>
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Query Match

Best Loc Matches

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Gene: jhp1117

Query Match

1;

Gaps

S.

Length 49;

Score 44.5; DB 2; Pred. No. 1e+03;

C, Keywords: chloroplast

4; Mismatches

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23 YKKKDQKQIKK----KRRKKKTNKKEEKKKK 49
                                                                                                                                                                                                     4 YAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKK
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Job time : 39 secs
                                                                 Query Match
Best Local Similarity 37.5%;
Matches 12; Conservative 4
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A,Title: Phylogenetic relationships among Tetrahymena species determined using the polym A,Reference number: S10259; MUID:90219078; PMID:2129541 A,Reference number: S10263 A,Stocession: S10263 A,Stocession: S10263 A,Status: nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NiAlternate names: scylliorinine S4
C;Species: Scyliorhinus canicula (smaller spotted catshark, smaller spotted dogfish)
C;Date: 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 09-Jul-2004
C;Accession: A41270; S12285
R;Sautiere, P.; Gusse, M.; Briand, G.; Martinage, A.; Chevaillier, P.
Biochim. Biophys. Acta 791, 82-86, 1984
A;Title: Primary structure of scylliorhinine S4, a protamine isolated from sperm nuclei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, COOST-LEGEROLOS: UNIPROT: P30259
R, Gusse, M.; Sautiere, P.; Chauviere, M.; Chevaillier, P.
Bjochim. Biophys. Acta 748, 93-98, 1983
A, Title: Extraction, purification and characterization of the sperm protamines of the A, Reference number: S01463; MUID: 84000513; PMID: 6615852
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C; Genetics:
                                                                                                                         A;Nolecule type: DNA
A;Residues: 1-41 <BRU>
A;Cross-references: UNIPROT:P17319; EMBL:X17128
A;Note: this sequence was submitted to the EMBL Data Library, November 1989
C;Genetics:
A;Genetics: A;Genetics: Code: SGC5
C;Superfamily: histone H3
C;Keywords: chromosomal protein; DNA binding; nucleosome core; nucleus
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C;Species: chloroplast Chlorella vulgaris
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
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16.7%; Score 44.5; DB 2; Length 32;
Best Local Similarity 41.4%; Pred. No. 7.5e+02;
Matches 12; Conservative 5; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 17.3%; Score 46; DB 2; Length 41; Best Local Similarity 44.8%; Pred. No. 6.8e+02; Matches 13; Conservative 3; Mismatches 13; Indels
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A;Molecule type: DNA
A;Residues: 1-49 <WAK>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protamine S4 - smaller spotted catshark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Residues: 1-5 <GUS>
C;Keywords: DNA binding; sperm; testis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Status: preliminary
A,Molecule type: protein
A,Residues: 1-32 <SAU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C,Genetics:
A;Genome: chloroplast
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
A41270
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

June 3, 2005, 10:19:18; Search time 171 Seconds (without alignments) 167.698 Million cell updates/sec

US-10-792-311-3 266 1 AKKYAKKEKAYAKKAEKAAK......EAKYKAEAAKAAAKEAAYEA 56 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 segs, 512079187 residues Searched:

85213 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 56

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

..

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	•	Description	Q6mgw9 bdellovibri	P11860 mytilus cal	Q71iy2 lactobacill	Q9df18 myoxocephal		Q7rf81 plasmodium		Q747m3 geobacter s	Q74cw2 geobacter s			_		Q9zk25 helicobacte		Q983t3 rhizobium l	Q7sia2 cricetulus	Q88un5 lactobacill	Q96rt9 homo sapien	-		Q25210 junonia coe	Q6ry82 pongo pygma	Q6ry92 pan troglod	Q6ry94 macaca fasc	_	Q81tc9 bacillus an	Q8n6f0 homo sapien		P83638 phyllomedus	Q71ipl lactobacill
		ID	Обмам	PHI3 MYTCA	Q711 <u>Y</u> 2	Q9DF18	ANP8 MYOSC	Q7RF81	MAR3 LEIMA	Q747M3	Q74CW2	ANP8 MYOAE	Q6F1 <u>A</u> 3	097314	Q6L0J1	Q9ZK25	оэтмн6	Q983T3	SYEP_CRIGR	Q88UNS	Q96RT9	Q7YV63	049175	Q25210	Q6RY82	Q6RY92	Q6RY94	Q84ZD8	Q81TC9	Q8N6F0	Q8IF74	DDSK_PHYDS	Q711F1
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		Match Length	43	45	44	42	45	51	23	35	37	40	54	54	48	54	51	24	49	52	42	53	26	42	44	44	44	52	38	55	42	33	20
æ	Query	Match	28.2	25.8	25.6	24.2	22.9	22.7	22.4	22.2	21.6	21.1	20.9	20.5	19.9	19.9	19.7	19.7	19.4	19.4	19.2	19.2	19.2	18.8	18.4	18.4	18.4	18.4	18.0	18.0	17.9	17.7	17.7
		Score	75	68.5	69	64.5	61	60.5	59.5	59	57.5	26	55.5	54.5	53	23	52.5	52.5	51.5	51.5	51	51	51	20	49	49	49	49	48	48	47.5	47	47
	Result	00	1	7	٣	4	S	9	7	œ	σ,	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31

	Q7tps2 mus musculu	-	P17319 tetrahymena	Q9arn7 oryza sativ		_		P82130 spinacia ol	07sic4 pseudopleur	Q9v779 drosophila	Q9uas9 boophilus m	Q7reb3 plasmodium	Q6ry93 canis famil
			8										
Q8T3J6	Q7TPS2	Q853H1	H32 TETBC	Q9ARN7	Q6MJ07	Q887D2	Q62WUS	P82130	Q7SIC4	Q9V779	Q9UAS9	O7REB3	Q6RY93
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46	22	39	40	47	48	53	22	34	38	54	38	41	44
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17	17	17	17	17	17	17	17	17	17	17	16	16	16
s.	46.5	46	46	46	46	46	46	45.5	45.5	45.5	45	45	45
46	•												

ALIGNMENTS

PRESULT. 1 10 G6KGM9 10 G6KGM9 11 G6KGM9 12 G6KGM9 12 G6KGM9 13 G6KGM9 14 G6MCM9 15 G6-JUL-2004 (TrEMBLrel. 27, Created) 15 G-JUL-2004 (TrEMBLrel. 27, Last sequence update) 16 G-JUL-2004 (TrEMBLrel. 27, Last sequence update) 17 G5-JUL-2004 (TrEMBLrel. 27, Last sequence update) 18 G-JUL-2004 (TrEMBLrel. 27, Last sequence update) 18 G-JUL-2004 (TrEMBLrel. 27, Last sequence update) 18 GA-GAMCMAN MAN MAN Macteration of Man Marches and M	d) equence update) motation update) motation update) separation update) separation update) separation update) feobacteria; Bdellovibrionales; Goesmann A., Meyer F., feobagenann A., Meyer F., smatches 15; Indels 2; Gaps 1; akrkakaakaaakaakaas 33 feobagenanta A. feobagena
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4912 MW;

45 AA;

SEQUENCE Query Match

VARIANT VARIANT

VARIANT VARIANT VARIANT Local Similarity 41.2 1es 21; Conservative

Matches

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PRELIMINARY;

Q711Y2

RESULT 3 2711Y2

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Gaps
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                                                    MEDINE=21192197; PubMed=11136728; DOI=10.1074/jbc.M009293200; Low W.-K., Lin Q., Stathakis C., Maio M., Fletcher G.L., Hew C.L.; Isolation and characterization of skin-type, type I antifreeze polypeptides from the longhorn sculpin, Myoxocephalus octodecemspinosus.";
J. Biol. Chem. 276:11582-11589(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Scorpaeniformes,
Cottoidei, Cottidae, Myoxocephalus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIINE=85285003; PubMed=4029130;
Hew C.-L., Joshi S., Wang N.-C., Kao M.H., Ananthanarayanan V.S.;
Skructures of shorthorn sculpin antifreeze polypeptides.";
Eur. J. Biochem. 151:167-172 (1985).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Myoxocephalus scorpius (Shorthorn sculpin) (Daddy sculpin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches 17; Indels
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PIR; A05163.
Antifreeze protein, Direct protein sequencing; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 AYAKKAEKAAKKAEAKAYKAAEAKKKAEAKYKAEAAKAAAK 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 APAKAAAKTAADAKAAAKTA-ADALAAANKTAAAAKAAAK 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4006 MW; 260C0BCC663B6878 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -! - SIMILARITY: Belongs to the type-I AFP family.
                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 24.2%; Score 64.5; DB 2; Similarity 53.7%; Pred. No. 1.1e+02; 22; Conservative 1; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 61; DB 1;
Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-MAR-1987 (Rel. 04, Created)
20-MAR-1987 (Rel. 04, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.9%;
Local Similarity 47.4%;
les 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26,
26,
26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antifreeze peptide SS-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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01-MAR-2004 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
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Name=PY04827;
                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE=Skin;
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=8097;
                               TISSUE=Skin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANP8 MYOSC
P04368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                              (possible variant of component I)
                    -i - FUNCTION: Involved in muclear basic protein transition: histones are replaced by spermatid specific proteins which are themselves replaced by protamines in late spermatids.
-i - SUBCELLULAR LOCATION: Nuclear.
-i - MISCELLANBOUS: The sequence of component I is shown.
-i - SUBARS 504941.
-i - SUBARS 510545.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                     component
component
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Myoxocephalus octodecimspinosis (Longhorn sculpin).

Myoxocephalus octodecimspinosis (Longhorn sculpin).

Myoxocephalus octodecimspinosis (Longhorn sculpin).

Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei, Acanthomorpha, Acanthopterygii, Percomorpha, Scorpaeniformes, Cottoidei, Cottidae, Myoxocephalus.

[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 AKRSPRKKKAAVKKSSK-----SKAKKPKSPKKKKAAK---KPAKKAAKK 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKYKAEAKAAAKE 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                                      protein sequencing; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 68.5; DB 1; Length 45;
                                                                                                                                                                                                                                                                              e core; Spermatogenesis.
S -> T (possible variant of cc
A -> T (in component II).
S -> T (possible variant of cc
S -> T (possible variant of cc
K -> R (possible variant of cc
K -> R (in component III).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25.6%; Score 68; DB 2; Length 44; 43.2%; Pred. No. 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Histone-like protein (Fragment).
Lactobacillus delbrueckii (subsp. lactis).
Bacteria: Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus
NCBI_TaxID=29397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SECUENCE FROM N.A.
STRAIN=ATCC 4797;
Langenheim J.F., Ulrich R.L.;
Submitted (WAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF496145; AAQ06805.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44 AA; 4634 MW; CAC365D7CFC6A162 CRC64;
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
  Eur. J. Biochem. 182:569-576(1989)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25.8%;
                                                                                                                                                                                                                                                   Chromosomal protein; Direct
Nuclear protein; Nucleosome
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19; Conservative

Local Similarity

Best Loca Matches

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Query Match

SEQUENCE

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AC DOT POT PRINCE REPORT REPOR

PRELIMINARY;

Q9DF18;

Q9DF18

RESULT 4 Q9DF18

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EMBL; AE017180; AAR36633.1; -.
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53.1%;
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5708 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 302:1967-1969(2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OrderedLocusNames=GSU3242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Geobacteraceae; Geobacter.
NCBI_TaxID=35554;
                                                                                                                                                                                                               Local Similarity 40.99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Geobacter sulfurreducens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein
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                                                                                                                                                 53 AA;
      environments."
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05-JUL-2004
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SEQUENCE
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REPEAT
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Q74CW2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1,
                                                                                                                                                                                                                                                                                                                                                        "Genome sequence and comparative analysis of the model rodent malaria parasite Plasmodium yoelii yoelii."; Nature 419:12-519(2002).
-I- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Membrane antigen containing repeating peptides (Clone 39) (Fragment).
Leishmania major.
Euskaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
                                                                                                                                        Carlton J.M., Angiuoli S.V., Suh B.B., Kooji T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.B., Selengut J.D., Koo H.L., Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bladwell S.L., Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M., Plorens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., Van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDILINE-88061089; PubMed-3502718;
Wallis A.B., McMaster W.R.;
"Identification of Leishmania genes encoding proteins containing
tandemly repeating peptides.";
J. Exp. Med. 166:1814-1824(1987).
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                      Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22.7%; Score 60.5; DB 2; Length 51; 42.1%; Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (OCT-1989) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 X 10 AA tandem repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
SEQUENCE 51 AA; 6414 MW; 8D6262526CE4C76F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 KKQKRKKKKKKMQKKRKSGKQREREREK-AEKKKEREKK 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 KKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAK 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53 AA.
                                                                                                                             PubMed=12368865; DOI=10.1038/nature01099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        preliminary data.
EMBL; AABL01001490; EAA16745.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X06556; CAA29799.1; -. PIR; PT0028; PT0028.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antigen; Membrane; Repeat.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
  Plasmodium yoelii yoelii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ×53
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                                                                                 SEQUENCE FROM N.A.
                                            NCBI_TaxID=73239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                        Carucci D.J.;
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STRAIN=PCA / ATCC 51573;
PubMed=14671304; DOI=10.1126/science.1088727;
PubMed=14671304; DOI=10.1126/science.1088727;
PubMedup a.A., Nelson K.B., Eisen J.A., Paulsen I.T., Nelson W.C.,
Heidelberg J.F., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J.,
Madupu R., Brinkac L.M., Daugherty S.C., DeBey R.T., Durkin A.S.,
Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,
Davidsen T.M., Zafar N., White O., Tran B., Romero C., Forberger H.P.
Weidman J.F., Khouri H.M., Feldblyum T.V., Utterback T.R.,
"Genome of Geobacter sulfurreducens: metal reduction in subsurface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
OrderedLocusNames=GSU1559;
Geobacter sulfurreducens.
Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
Geobacteraceae; Geobacter.
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                                                                                                                                                                                                                                          DB 1; Length 53;
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                                                                                                                                                                                                                                                                                             10; Indels
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                                                                                                                                                                                                                                                                                                                                                  14 KAEKAAKKAEAKAYKAAEAKKKAE--AKYKAEAAKAAAKEAAYE
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SEQUENCE 35 AA; 3966 MW; 0E6E2B600A034777 CRC64;
                                                                                                                                                                                     75D264BB078C06C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 27, Last sequence update) (TrEMBLrel. 27, Last annotation update)
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Last annotation update)
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Pred. No. 2.6e+02;
                                                                                                                                                                                                                                        22.4%; Score 59.5; DB 1;
40.9%; Pred. No. 3.4e+02;
live 13; Mismatches 10
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6 (partial).
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MEDLINE=22255708; PubMed=12368867; DOI=10.1038/nature01095;
MEDLINE=22255708; PubMed=12368867; DOI=10.1038/nature01095;
Hall N., Bearman M., Churcher C., Harris B., Harris D.,
Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
Mungall K., Bowman C., Cherevach I., Chillingworth C.,
Chillingworth T., Christodoulou Z., Clark L., Clark R.,
Cornin A., Davies R., Davis P., Dearden F., Doggett J.,
Cronin A., Davies P., Dars P., Dearden F., Doggett J.,
Reltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,
R. Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
R. Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,
Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
Inte A., Maddison M., Mclean J., Mooney P., Moule S., Murphy L.,
Oliver K., Ormond D., Price C., Quail M.A., Rabbinowitsch E.,
A geger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,
Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
Sulston J.E., Craig A., Newbold C., Barrell B.G;
"Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE = 99376085; PubMed=10448855; DOI=10.1038/22964;
Bowman S., Lawson D., Basham D., Brown D., Chillingworth T.,
Bowman S., Lawson D., Basham D., Brown D., Chillingworth T.,
Churcher C.M., Craig A., Davies R.M. Devlin K., Feltwell T.,
Gentles S., Gwilliam R., Hanlin N., Harris D., Holroyd S., Hornsby T.,
Horrocks P., Jagels K., Jassal B., Kyes S., McLean J., Moule S.,
Mungall K., Murphy L., Oliver K., Quall M.A., Rajandream M.A.,
Rutter S., Skelton J., Squares R., Squares S., Sulston J.E.,
Whitchead S., Woodward J.R., Newbold C., Barrell B.G.;
"The complete nucleotide sequence of chromosome 3 of Plasmodium
                                                                                                                                                     Birren B.W., Stange-Thomann N., Hafez N., DeCaprio D., Fisher S.,
Butler J., Elkins T., Kodira C.D., Major J., Wang S., Nicol R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein MAL3P7.36 (F49c12.11-like protein).
Name-MAL3P7.36; Synonyms=PFC13B7.39
Plasmodium falciparum (isolate 3D7).
Eukaryota, Alveolata, Apicomplexa, Haemosporida; Plasmodium.
                                                                                                                                                                                                 Nusbaum C.;
Submitted (UUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AE017263; AAT75720.1;
GO; GO:0005523; C:intracellular; IEA.
GO; GO:0003735; F:structural constituent of ribosome; IEA.
GO; GO:0003735; P:structural constituent of ribosome; IEA.
GO; GO:0006412; P:protein biosynthesis; IEA.
InterPro; IPR001911; Ribosomal_S21.
TIGRPAMs; TIGR0003; S12p; 1.
Complete proteons; Ribosomal protein.
SEQUENCE 54 AA; 6492 MW; A429E0AD37C39E95 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 OKVASSNKAEARKREYHLSKKEKRIY----KQKQNRKYK 54
Bacteria, Firmicutes, Mollicutes, Entomoplasmatales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKYK 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 55.5; DB 2;
Pred. No. 7.3e+02;
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                            Entomoplasmataceae; Mesoplasma
NCBI_TaxID=2151;
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37.5%;
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                                                                                                                                STRAIN=L1 / ATCC 33453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                   SEQUENCE FROM N.A.
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                  PubMed=14671304, DIC=10.1126/science.1088727;
PubMed=14671304, DIC=10.1126/science.1088727;
PubMed=14671304, DIC=10.1126/science.1088727;
PubMed=14671304, DIC=10.1126/science.1088727;
Heidelberg J.E., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J., Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S., Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J., Davidsen T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A. Weidman J.F., Khouri H.M., Feldblyum T.V., Utterback T.R., Weidman J.E., Lovley D.R., Fraser C.M.;
"Genome of Geobacter sulfurreducens: metal reduction in subsurface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chakrabartty A., Hew C.-L., Shears M., Fletcher G.;

"Primary structures of the alamine-rich antifreeze polypeptides from grubby sculpin, Myoxocephalus aenaeus.";

Can. J. Zool. 66:403-408 (1988).

-!- FUNCTION: Antifreeze proteins lower the blood freezing point.

-!- SIMILARITY: Belongs to the type-I AFP family.

PIR; S07046; FDF18G.

Antifreeze protein; Direct protein sequencing; Repeat.

MOD RES

1 Blocked amino end (Met).

SEQÜENCE 40 AA; 3579 MW; 32F50EE243C2ADII CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Būkaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          21.6%; Score 57.5; DB 2; Length 37; 48.6%; Pred. No. 3.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                 Complete proteome; Hypothetical protein.
SEQUENCE 37 AA; 4015 MW; B7E38FAFD5F3SA77 CRC64;
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Last annotation update)
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50.0%; Pred. No. 5.1e+02;
tive 3; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 KKEKAYAKKAEKAAKKA-EAKAYKAAEAKKKAEAK 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Antifreze peptide GS-8.
Myoxocephalus aeneeus (Grubby sculpin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Mismatches
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                                                                                                                                                                                                                                                                                                                               EMBL; AE017180; AAR34933.1; -.
TIGR; GSU1559; -.
                                                                                                                                                                                                                                                                                                     Science 302:1967-1969(2003).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48.68;
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Matches 17; Conservative
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nes 17; Conservative
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10 06 F1A3 06 P1A3 06 P1A 25 06 P1A

RESULT 11

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Gaps

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Length 54;

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Indels

2; Mismatches

Score 53; DB 2; Length 54; Pred. No. 1.2e+03;

96C37ACAB155C35C CRC64;

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10 AYAKKAEKAAKKAEAKAYKAABAKKKAEAKYKAEAA 45
 EMBL, AE001539; AAD06698.1; -. PIR; F71847; F71847. POMPLee proteome. SEQUENCE 54 AA; 5873 MW; 91
                                                                      19.9%;
                                                                                                    15; Conservative
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                                                                                     Similarity
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Fuetterer O., Angelov A., Liesegang H., Gottschalk G., Schleper C.,
Schepers B., Dock C., Antranikian G., Liebl W.;
"Genome sequence of Picrophilus torridus and its implications for life
                                                                                                  Gaps
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Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown B.D., Doig P.C.,
Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
Trust T.J.;
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Nature 397:176-180(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
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                                                                    / Match 20.5%; Score 54.5; DB 2; Length 54; Local Similarity 44.4%; Pred. No. 8.8e+02; nes 20; Conservative 3; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                            Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
Picrophilaceae; Picrophilus.
NCBI_TaxID=82076;
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                                                                                                                             13 KKAEKAAKKA-----EAKAYKAAEA-KKKAEAKYKAEAAKAAAK
                                                                                                                                               10 KKPLKAAKKGPVELTEEDIAFKKEMAEKKKAEEEAKOKLLKAKKK
Nature 419:527-531(2002).
EMBL; AL034559; CAB39063.1; -.
Hypothetical protein.
SEQUENCE 54 AA; 6065 MW; E24DBCEB3DE2492B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 101:9091-9096 (2004).
EMBL, AE017261; AAT43511.1; -.
COMDLE Protecome; Hypothetical protein.
SEQUENCE 48 AA; 5394 MW; A08C0B6BEFFA99D5 CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Putely motility protein.
OrderedLocusNames=JHP1117;
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Last annotation update)
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KEDKKKEKEFLKKIRKNSIKSDDIAEDAAAAEEDA 38
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NCBI_TaxID=85963;
                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=DSM 9790 / ATCC 700027;
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                                                                                                                                                                                                                                                                                                     Hypothetical protein.
OrderedLocusNames=PT00926;
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MEDILMES90237237; PubMed=1692037;
KObhaaka H., Yamamoto K., Fujii H., Miura H., Miyaaaka N., Nishioka K.,
Miyamoto T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Fine epitope mapping the human SS-B/La protein: Identification of distinct autoepitope homologous to a viral gag polyprotein."; J. Clin. Invest. 85:1566-1574(1990).
EMBL. M35263; AAA36653.1; -.
                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 1.2e+03;
5; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 AA; 6218 MW; EA152B8386E7F078 CRC64;
                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) SS-B/La protein (Fragment).
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51 AA
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Local Similarity 42.1%;
hes 16; Conservative
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OM protein - protein search, using sw model

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3, 2005, 10:20:03 ; Search time 157 Seconds (without alignments) 137.953 Million cell updates/sec

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Title: Perfect score:

26

1 AKKYAKKEKAYAKKAEKAAK......EAKYKAEAAKAAAKEAAYEA Sequence:

Gapop 10.0 , Gapext 0.5

BLOSUM62

Scoring table:

2105692 seqs, 386760381 residues Searched:

Total number of hits satisfying chosen parameters:

DB seq length: 0 DB seq length: 56 Minimum Maximum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

A_Geneseq_16Dec04:* 1: geneseqp1980s:* ..

geneseqp1980s:*

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp1990s:* geneseqp2000s:* geneseqp20018:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

SUMMARIES

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	Copolymer	Copolymer	Copolymer	eic a	High affi	ide u	catio	Protamine	Polycatio	Protamine	ide m	ide u	Polycatio	Protamine	Polycatio	Polycatio	Protamine	Protamine	Histone H	Human his	ide m	ide u	Polycatio	Protamine	tic d
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Description	2573	2572	2571	4449		Ado43176	Aar90180	Aaw06686	0181	Aaw06688	Aab08170	Ado43172	Aar90179	Aaw06698	Aar90178	0176	Aaw06687	Aaw06697	Aay34069	7367	Aab08169	Ado43179	0177	6685	4719
Desc	Aay82573	Aay82572	Aay82571	Aaw24449	Aar28871	Ado4	Aar9	Aaw0	Aar90181	Aawo	Aab0	Ado4	Aar9	Aaw0	Aar9	Aar90176	Aaw0	Aaw0	Aay3	Aay57367	Aabo	Ado4	Aar90177	Aaw06685	Aar74719
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& Query Match	100.0	50.6	9.3	5.2	3.6	3.3	1.6	1.6	1.6	1.6	31.0	1.0	6.6	29.9	29.7	7.6	29.7	7.6	28.8	28.8	28.4	8.2	7.8	27.8	7.8
₩ Š ĕ	ä	Ñ	m	m	m	m	m	m	'n	m	m	m	53	Ñ	7	N	N	N	Ñ	Ñ	7	Ñ	'n	'n	27
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Aar64798 Amphipath Aar77070 Synthetic Aar92400 Lytic pep Aar90754 Synthetic Aaw08401 Nucleic a Aaw69205 Nucleic a Aaw44934 Mycobacte Adf5561 Methylate Adf5561 Methylate Adf5561 Methylate Adf3561 Delivery Aaw38815 Delivery Aaw38815 Delivery Aaw38816 Delivery Aaw38816 Delivery Aaw38816 Delivery Aaw38816 Delivery Aaw38916 Delivery Aaw38916 Delivery Aaw38919 Peptide u Aay59038 Peptide #	Aab45846 Nucleic a Aau04283 Trimeric Aau18248 Novel hum
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444444000000000000000000000000000000000	72 72 71.5
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ALIGNMENTS

Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyrodi; antinflammatory; antidabetic; thyromimetic; antidabetic; antidabetic; thyromimetic; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; cronn's disease; orronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; pemphigus vulgaris; systemic lupus erythematosus. Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:3. AAY82573 standard; peptide; 56 AA. (first entry) 28-JUL-2000 RESULT 1

Unidentified

WO200018794-A1.

06-APR-2000.

99WO-US022402. 24-SEP-1999; 98US-0101693P. 25-SEP-1998; (YEDA) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.

Gad A, Lis D;

WPI; 2000-317499/27.

Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.

Claim 10; Page 14; 72pp; English.

AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention of escribes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides

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treating and preventing immune diseases in a mammal. Autoimmune diseases

treating and preventing immune diseases in a mammal. Autoimmune diseases

treating and preventing immune diseases in a mammal. Autoimmune diseases

diseases Such diseases include arthritic conditions, demyelinating

diseases Such diseases include arthritic conditions, demyelinating

diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid

arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune

cophoritis, autoimmune thyroiditis, autoimmune thyroidmines, disease, chronic immune thyroidmines, Graves disease, Guillain-Barre's

shadinote, Hashimoto's disease, idiopathic myrosdema, myasthenia gravis,

syndrome, Hashimoto's disease, idiopathic myrosdema, myasthenia gravis,

psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-
mediated diseases which can be treated include host-versus-graft disease,

psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-
mediated diseases, and delayed-type hypersensitivity. The

polypeptides of the invention have defined molecular weights and physical

properties which are analogous to glatiramer acetate molecules, which

makes them ideal for use as molecular weight markers
invention are used as molecular weight markers for glatiramer
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                                                0; Gaps
                                                                                        1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKYKAEAAKAAAKEAAYEA 56
100.0%; Score 266; DB 3; Length 56; 100.0%; Pred. No. 7e-20; ive 0; Mismatches 0; Indels
Query Match
Best Local Similarity 100.0
Matches 56; Conservative
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AAY82572 standard; peptide; 45 AA. AAY82572;

28-JUL-2000 (first entry)

Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:2.

glatiramer acetate, autoimmune disease, antiarthritic, neuroprotective, osteopathic, immunosuppressive, antithyroid, antiinflammatory; antidiabetic; thyromimetic; haemostatic; antipsoriatic, dermatological, antianaemic; immunosuppressive, demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Copolymer; molecular weight marker; TV-marker; immune disease; disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus. Hashimoto's

Unidentified

WO200018794-A1.

06-APR-2000.

99WO-US022402. 24-SEP-1999; ..

98US-0101693P.

25-SEP-1998;

(YEDA) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.

Lis D; Gad A, WPI; 2000-317499/27.

Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases

Claim 10; Page 14; 72pp; English

AAY82571 to AAY82577 represent specifically claimed copolymer molecular

Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.

(YEDA) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.

WPI; 2000-317499/27.

Gad A, Lis D;

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invention describes polypeptides (T) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatizamer acid composition are used as molecular weight markers for glatizamer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune attentions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune thrombocytopaenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Gillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, psoriasis, pempidus vulgaris, or systemic lupus erythematosus. Mediated mediated diseases which can be treated include host-versus-graft disease, and delayed-type hypersensitivity. The groupserties which are analogous to glatizamer acetate molecules, which makes them ideal for use as molecular weight markers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              syndrome; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acceate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory antidiabetic; thyromimetic; haemostatic; antipsoriatic dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; theumatoid arthritis; crohis disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; duillain-Barre's syndrome; psoriasis Hashimoto's disease; idiopathic myxoedems; myasthenia gravis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKY-KAEAAKAAKEAAYEA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   weight TV-marker polypeptides from the present invention. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 134.5; DB 3; Length 45;
Pred. No. 1.1e-06;
0; Mismatches 5; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pemphigus vulgaris; systemic lupus erythematosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY82571 standard; peptide; 35 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 45 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :5-SEP-1998;
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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer actatate invention are used as molecular weight markers for glatiramer actatate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune thyroidmune haemolytic anaemia, autoimmune thyroidmune baemolytic anaemia, autoimmune cophoritis, autoimmune thyroidmune seen of disease, chronic immune thyroidmines, graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic mysocedema, mysathenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythemacosus. Mediated mediated diseases which can be treated include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The properties which are analogous to glatiramer acetate molecules, which are analogous to glatiramer acetate molecules, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW24434-W24459 are nucleic acid (NA) binding peptides, capable of both condensing and stabilising a NA. The peptides can be conjugated to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid transporter; gene therapy; binding complex; lysis agent; JTS-1; K8; alpha helix; endosome; lysosome; nucleus targeting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKYKAEAAKAAAKEAAYEA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid transporter useful in gene therapy - contains binding complex associated with surface and nuclear ligands and lysis agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid (NA) binding peptide used in NA delivery to cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39.3%; Score 104.5; DB 3; Length 35; 51.8%; Pred. No. 0.0009; tive 4; Mismatches 2; Indels 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 49; 125pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW24449 standard; peptide; 46 AA
                   Claim 10; Page 14; 72pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-052345/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 35 AA;
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lytic peptide to form a nucleic acid transporter system. The lysis agent forms an alpha-helical structure. The transporter system is used to deliver nucleic acid to a cell and for treating humans by gene therapy. By taking advantage of the characteristics of both the lysis agents and the binding molecules, delivery of the nucleic acid is enhanced. Specific lysis agents are capable of releasing the nucleic acid into the cellular interior from the endosome. Release is efficient without endosomal/lysosomal degradation. Once released the binding complexes help target the nucleic acid to the nucleus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       glycopeptide; mannose; mannosylated; glycosylated; mannose receptor; macrophages; monocytes; destroy; cytotoxicity; label; image; alter; macrophage processing of antigen; MHC restriction; inflammation; inflammatory diseases; macrophage secretory products; Crohn's disease; legionnaires disease; mononuclear phagocytes; HIV; AIDS; lysosomal storage diseases; Gaucher's disease, asthma; alveolar macrophages metastasis; systemic macrophages; deliver; antigenic peptides; prevent transplant rejection; organ transplantation; antitumour agents; cancer; toxins.
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28
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glucosamine. May also have non interfering substits."
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                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High affinity macrophage mannose receptor ligand compound #9.
                                                                                                                                                                                               35.2%; Score 93.5; DB 2; Length 46; 60.5%; Pred. No. 0.015; Live 4; Mismatches 12; Indels
                                                                                                                                                                                                                                                              9 KAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKYKAEA-AKAAAK 50
                                                                                                                                                                                                                                                                                 fucose,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "opt may have mannose,
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                                                                                                                                                                                                                                                                                                                                                                               AAR28871 standard; peptide; 46
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                                                                                                                                                                                                                                26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             (revised)
                                                                                                                                                                                                                 Similarity
                                                                                                                                                                  Sequence 46 AA;
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Nano-barcode; scanning probe microscopy; probe.

22-SEP-2003; 2003WO-US029726. 20-SEP-2002; 2002US-00251152. 19-SEP-2003; 2003US-00667004.

WO2004038037-A2.

Synthetic.

06-MAY-2004.

Peptide used for coded probe synthesis.

(first entry)

29-JUL-2004

ADO43176;

ADO43176 standard; peptide; 56 AA.

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This compound represents a glycopeptide effective in inhibiting the binding of labelled mannosylated BSA to mannose receptors. Mannose receptors are uniquely found on macrophages and not on monocytes. Glycopeptides are uniquely found on macrophages and morocytes. Glycopeptides such as this provide a mechanism to target macrophages specifically, to image, label, destroy or otherwise alter their antigen processing function. In addition they can be conjugated to solid supports and used to purify mannose receptors from a variety of sources. They are useful in the treatment of inflammatory diseases driven by macrophage secretory products eg. Crohn's disease; infectious diseases in which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            macrophages harbour replicating infectious agents eg. Legionnaires diseases, viral infections involving mononuclear phagocytes eg. HIV and lysosomal storage diseases, in which macrophages are principally involved eg. Gaucher's disease, asthma mediated by alveolar macrophages; and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New high affinity mannose receptor ligand cpds. - for treating diseases mediated by macrophage activity e.g. asthma, inflammatory diseases and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      controlling metastasis, mediated by systemic macrophages. The peptides can also be used to deliver antigenic peptides as conjugates to a macrophage to marshal an immune response; also self peptides to prevent issue transplant rejection. (Updated on 25-MAR-2003 to correct by
                                                                                                                                                                                                                                                                                                                                             /note= "opt may have mannose, fucose, glucose or N-Ac-
glucosamine. May also have non interfering substits."
 may have mannose, fucose, glucose or N-Ac-
                                         /note= "opt may have mannose, fucose, glucose or N-Ac-
glucosamine."
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glucosamine."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            infectious diseases, e.g. HIV.
                   glucosamine."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1992-398516/48.
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                                     Modified-site
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Detecting, identifying and sequencing of biomolecules using controlled alignment of nano-barcodes encoding specific information for scanning probe microscopy, useful in the fields of molecular biology.

Yamakawa M;

Su X,

Chan S,

(ITLC) INTEL CORP

WPI; 2004-399960/37.

Example 2; Page 44; 63pp; English.

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The present sequence is that of a peptide of potential use for production of a coded probe useful in the method of the invention. The invention provides methods, apparatus and compositions for the detection, identification and/or sequencing of bimolecules, such as nucleic acids or proteins. Coded probes comprising a probe molecule attached to one or more nano-barcodes are allowed to bind to target molecule(s). After binding and separation from unbound coded probes, the bound coded probes are allowed from unbound coded probes, the bound coded probes are allowed as surface and analysed by scanning probe microscopy (SPM). The methods allow the sequencing of long nucleic acid sequences in a single sequencing run, high speed of obtaining sequence data, low cost of sequencing and high efficiency in terms of operator time, and sensitive and accurate detection and/or identification of nucleic acids with low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 n-protamine; anticoagulation reversal; low molecular weight heparin; polycationic; positively charged amino acid; lysine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 AKKEKAYAKKAEKAAKKAEAKAYKAABAKKKAEAKYKAEAAKAAAKEAAYEA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33.3%; Score 88.5; DB 8; Length 56; 55.8%; Pred. No. 0.061; Live 1; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polycationic polypeptide n-protamine analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       incidence of false positive results.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR90180 standard; peptide; 32 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 56 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR90180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR90180
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8
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5

Gaps

Э,

33.6%; Score 89.5; DB 2; Length 46; 59.6%; Pred. No. 0.039; Live 4; Mismatches 12; Indels

duery Match Best Local Similarity 59.69 Matches 28, Conservative

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KYAKKEKAYAKKAEKAAKKAE-AKAYKAAEAKKKAEAKYKAEAAKAA

RESULT 6 ADO43176

ij

10-NOV-1994; 12-NOV-1993; 08-SEP-1994;

WO9513083-A1

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Protamine sulphate (also called n-protamine or salmine protamine) is a polycationic peptide derived from salmon sperm and is used to reverse heparin anticoagulation. One of the major components of salmine protamine is a 32 amino acid peptide having a total cationic charge of [+21], with arguine accounting for 67% of the total sequence and for all of the positive charge. Peptides of 20.40 amino acids with total cationic charge less than [+21] and which are able, at least partially, to reverse the offect of heparin and/or low molecular weight heparin anticoagulants are effect of heparin and/or low molecular weight heparin anticoagulants are claimed. Specifically, the peptides are polycationic analogues of n-correct protamine where the positive charge on the amino acid sequence is reduced by selective replacement of positively charged arguine residues with an uncharged residue, so that total cationic charge is less than [+21]. The can peptides are used in vivo to reverse the effects of heparin; they have the same anti-heparin activity as protamine but are less toxic (because of the reduced number of positive charges) and are relatively easy and inexpensive to prepare. The present sequence represents a specific example of a protamine-like peptide with a charge of [+18] which has been found to reverse the anticoagulation effects of both standard and low molecular weight heparin

    30
    /label= repeat_region
    /note= "4 tandem repeats of (Lys)2(Ala)2(Lys)2Ala motif"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide reversing the anticoagulant effects of heparin - is based on protamine but has fewer positive charges for reduced toxicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          n-protamine; anticoagulation reversal; low molecular weight heparin; polycationic; positively charged amino acid; lysine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.6%; Score 84; DB 2; Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKK 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polycationic polypeptide n-protamine analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wakefield TW, Stanley JC, Andrews PC;
                         Location/Qualifiers
                                                                                'note= "acetylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 5; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR90181 standard; peptide; 33 AA
                                                                                                                                                                                                                   /note= "amidated"
                                                                                                                                                                                                                                                                                                                                                                                      96WO-US006567.
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Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UNMI ) UNIV MICHIGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-011697/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 32 AA;
                               Key
Modified-site
                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                      08-MAY-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  determined by the number of positively charged amino acids in the sequence. Preferably the positive charges are grouped in clusters sequence. Preferably the positive charges are grouped in clusters sequence. Preferably the positive charges are grouped in clusters sequence. Preferably the positive charges are proposed in clusters amino acids having blocks of 2-4 positively charged amino acids separated by neutral acids. Alternatively the positive charge may be distributed evenly or randomly along the peptide sequence. In particular the peptides are analogues of n-protamine (total cationic charge = +21) in which selected arginine residues have been replaced by other positively charged amino acid residues have been replaced by other positively charged amino acid residues have been replaced by other positively charged amino acid residues have been replaced by other positively charged amino acid residues have been replaced by cherr positively charged amino acid residues have been replaced by the positively charged amino acid residues have been replaced by the positively contrained argumentation and the malogues of low mol. Wt. heparin (LMMH) anticoagulation and protamine since the reduced positive charge gives an improved efficiency to toxicity ratio; and they may be more effective than n-protamine in their anti-LMMH action. The present sequence (total cationic charge = 18) is a specific example of the new polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Coagulation; anticoagulant; heparin; platelet aggregation; cell adhesion; positively charged cluster; arginine; polycationic; decrease; n-protamine; salmine protamine; protamine sulphate; salmon sperm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel peptides are claimed which contain 20-40 amino acids and which have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New poly:cationic polypeptide n-protamine analogues - having reduced cationic charge and lower toxicity, used for reversing (low mol.wt.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 31.6%; Score 84; DB 2; Length 32; Local Similarity 62.9%; Pred. No. 0.096; les 22; Conservative 3; Mismatches 6; Indels
                                                                                                         /note= "C-terminal is in amide form"
                                                      'note= "N-terminal is acetylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKK 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protamine-like peptide analogue [+18B].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Andrews PC;
Location/Quálifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 13; 34pp; English
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                                                                                                                                                                                                                                                                          94WO-US012981.
                                                                                                                                                                                                                                                                                                                                93US-00152488.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    heparin anticoagulation.
                                                                                                                                                                                                                                                                                                                                                                                                           (UNMI ) UNIV MICHIGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1995-193899/25.
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  Key
Modified-site
                                                                             Modified-site
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Gaps

4,

05-AUG-1997

AAW06686;

RESULT 8

Query Match

Best Loc Matches

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Synthetic

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Sequence 33 AA;
                                                                                            Modified-site
                                                                                                                                                                                                                Modified-site
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                          Synthetic.
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and low mo
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                                                                                                                                               Region
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    ZXEXEXEXEX BX BX B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a total cationic charge of less than +21 (pref. +16 to +18) esp. +18) as determined by the number of positive charged amino acids in the sequence. Preferably the positive charges are grouped in clusters separated by neutral amino acids. Especially the peptides contain 28-32 amino acids having blocks of 2-4 positively charged amino acids separated by blocks of 2-6 neutral acids. Alternatively the positive charge may be distributed evenly or randomly along the peptide sequence. In particular the peptides are analogues of n-protamine (total cationic charge = +21) in which selected arginine residues have been replaced with uncharged amino acids and other arginine residues have been replaced by other positively charged amino acid residues, preferably lysine. The peptides reverse the effect of low mol. Wt. heparin (LMMH) anticoagulation and hence can be used medically to prevent bleeding after the conclusion of clinical procedures using heparin therapy. They are less toxic than n-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Coagulation; anticoagulant; heparin; platelet aggregation; cell adhesion; positively charged cluster; arginine; polycationic; decrease; n-protamine; salmine protamine; protamine sulphate; salmon sperm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel peptides are claimed which contain 20-40 amino acids and which have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protamine since the reduced positive charge gives an improved efficiency to toxicity ratio, and they may be more effective than n-protamine in their anti-LMWH action. The present sequence (total cationic charge =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New poly:cationic polypeptide n-protamine analogues - having reduced cationic charge and lower toxicity, used for reversing (low mol.wt.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 31.6%; Score 84; DB 2; Length 33; Local Similarity 62.9%; Pred. No. 0.1; es 22; Conservative 3; Mismatches 6; Indels
                                                                                                                                          /note= "C-terminal is in amide form'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             +16) is a specific example of the new polypeptides
                                                                                            /note= "N-terminal is acetylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||| ||| |||   ||   ||   |||   |||   |||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||   ||  
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protamine-like peptide analogue [+18BE].
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Andrews PC;
                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 13; 34pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW06688 standard; peptide; 33
                                                                                                                                                                                                                                                                                    94WO-US012981
                                                                                                                                                                                                                                                                                                                             93US-00152488
94US-00303025
                                                                                                                                                                                                                                                                                                                                                                                                                                               Wakefield TW, Stanley JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         heparin anticoagulation.
                                                                                                                                                                                                                                                                                                                                                                                                   (UNMI ) UNIV MICHIGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1995-193899/25
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                                                  Key
Modified-site
                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                    10-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                        08-SEP-1994;
                                                                                                                                                                                     WO9513083-A1
  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW06688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Matches
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WWW.EXTXRXD.
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Protamine sulphate (also called n-protamine or salmine protamine) is a polycationic peptide derived from salmon sperm and is used to reverse heparin anticosquiation. One of the major components of salmine protamine is a 32 amino acid peptide having a total cationic charge of [+21], with arginine accounting for 67% of the total sequence and for all of the arginine accounting for 67% of the total sequence and for all of the positive charge. Peptides of 20-40 amino acids with total cationic charge less than [+21] and which are able, at least partially, to reverse the effect of heparin and/or low molecular weight heparin anticoagulants are class than carried Specifically, the peptides are polycationic analogues of northannewhere the positive charge on the amino acid sequence is reduced by selective replacement of positively charged arginine residues with an uncharged residue, so that total cationic charge is less than [+21]. The numbarged residue, so that total cationic charge is less than [+21]. The have the same anti-heparin activity as protamine but are less toxic (because of the reduced number of positive charges) and are relatively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ï
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                                                                                                                                    4. .31
/label= repeat_region
/note= "4 tandem repeats of (Lys)2(Ala)2(Lys)2Ala motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide reversing the anticoagulant effects of heparin - is based on protamine but has fewer positive charges for reduced toxicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31.6%; Score 84; DB 2; Length 33; 62.9%; Pred. No. 0.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 AKKAAKKAKKAAKKAAKKAK----KAAKKAKK 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Andrews PC;
Location/Qualifiers
                                                                                   note= "acetylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 5; 42pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB08170 standard; peptide; 40 AA
                                                                                                                                                                                                                                                                                                  /note= "amidated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96WO-US006567.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wakefield TW, Stanley JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-DEC-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UNMI ) UNIV MICHIGAN
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Su X, Yamakawa M;
            (ITLC ) INTEL CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-SEP-1994;
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                                                                                                                                                                                                                                                                                                                                                                                            27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR90179;
                                Chan S,
                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a synthetic peptide which has a high affinity for glycoaminoglycans and proteoglycans. The peptide is useful in methods for modulating heparin or other glycoaminoglycans with anticoagulant activity, promoting cell attachment or adhesion to natural or synthetic surfaces (sepcially vein grafts), modulating tumour cell metastasis, modulating cartilage differentiation, targeting drugs to epithelial cell surfaces (or to other cells expressing proteoglycans), modulating enzymes that act on glycoaminoglycan substrates, affinity purification of bioactive sequences of a glycoaminoglycan, modifying endothelial cell pro-coagulant or anti-coagulant functions mediated through glycoaminoglycans, and modulating wound healing. The peptide may also be used for blocking tissue uptake of heparin or other
                                                                                                                                                                                                  Novel synthetic peptides with high affinity for glycoaminoglycans and proteoglycans, useful for modulating heparin, promoting cell attachment, modulating tumor metastasis and modulating wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
cell attachment, cell adhesion, vein graft; tumour cell metastasis; cartilage differentiation; wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2
                                                                                                                                                                                                                                                                                                                                                                                                                                              31.0%; Score 82.5; DB 3; Length 40; llarity 53.7%; Pred. No. 0.17; Conservative 5; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 KKAEKAAKKAEAKAYKAAEAKKKAEAKYKAEAAKAAAKEAA 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nano-barcode; scanning probe microscopy; probe.
                                                                                                                                                           Schick BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide used for coded probe synthesis.
                                                                                                                                                                                                                                             Disclosure, Page 30, 76pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADO43172 standard; peptide; 49 AA
                                                                                                                                                           Verrecchio A,
                                                                                                                                      (UYJE-) UNIV JEFFERSON THOMAS
                                                                                             12-FEB-2000; 2000WO-US002853.
                                                                                                                 99US-0118276P
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19-SEP-2003; 2003US-00667004
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                                                                                                                                                                                WPI; 2000-543446/49.
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nes 22; Conserv
                                                                                                                                                           San Antonio JD,
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                                                   WO200045831-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 40 AA;
                                                                                                                 )2-FEB-1999;
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                                Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Matches
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provinces meruncus, apprairation and compositions for the detection, dentification and/or sequencing of biomolecules, such as nucleic acids or proteins. Coded probes comprising a probe molecule attached to one or more nano-barcodes are allowed to bind to target molecule(s). After more nano-barcades are allowed to bind to target molecule(s). After inding and separation from unbound coded probes, the bound coded probes are aligned on a surface and analysed by scanning probe microscopy (SPM). An approach to coded probe synthesis entails creating polymer scaffolds to which nano-tag elements are attached through post-polymer assembly. For example, nano-tag elements can be attached to a peptide that has active groups (in the present case, lysine) at specific appropriately espaced sites. The peptide is then exposed to a mono-functionalised nanotag element and all of the active sites are modified. The methods allow the sequencing of long nucleic acid sequences in a single sequencing run, high speed of obtaining sequence data, low cost of sequencing and high efficiency in terms of operator time, and sensitive and accurate cated accurate cated and accurate cated c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is that of a peptide of potential use for production of a coded probe useful in the method of the invention. The invention provides methods, apparatus and compositions for the detection,
                                                                                                        Detecting, identifying and sequencing of biomolecules using controlled alignment of nano-barcodes encoding specific information for scanning probe microscopy, useful in the fields of molecular biology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        n-protamine; anticoagulation reversal; low molecular weight heparin; polycationic; positively charged amino acid; lysine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  з дадакдададкададакададкада - дакададакдадад 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polycationic polypeptide n-protamine analogue.
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                                                                                                                                                                                                                                                                                                                                                                       Example 2; Page 43; 63pp; English
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94US-00303025.
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Best Local Similarity
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WPI; 2004-399960/37
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New poly:cationic polypeptide n-protamine analogues - having reduced
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                                                                                                determined by the number of positively charged amino acids in the sequence. Preferably the positively charged amino acids in the sequence. Preferably the positively charged amino acids in the sequence. Preferably the positively charged amino acids in the sequence. Preferably the positively the positive contain 28-32 amino acids having blocks of 2-4 positively charged amino acids separated by blocks of 2-6 neutral acids. Alternatively the positive charge may be distributed evenly or randomly along the peptide sequence. In particular the peptides are analogues of n-protamine (total cationic charge = +21) in which selected arguine residues have been replaced by other positively charged amino acid residues have been replaced by other positively charged amino acid residues, preferably lysine. The peptides creverse the effect of low mol. Wt. heparin (LMWH) anticoagulation and charce can be used medically to prevent bleeding after the conclusion of clinical procedures using heparin therapy. They are less toxic than n-protamine since the reduced positive charge gives an improved efficiency to toxicity ratio; and they may be more effective than n-protamine in their anti-LMMH action. The present sequence (total cationic charge = +18) is a specific example of the new polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Coagulation; anticoagulant; heparin; platelet aggregation; cell adhesion; positively charged cluster; arginine; polycationic; decrease; n-protamine; salmine protamine; protamine sulphate; salmon sperm.
                                                                                        peptides are claimed which contain 20-40 amino acids and which have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3. .23
/label= repeat_region
/note= "3 tandem repeats of (Lys)2(Ala)2(Lys)2Ala motif"
            New poly:cationic polypeptide n-protamine analogues - having reduced cationic charge and lower toxicity, used for reversing (low mol.wt.)
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protamine-like peptide analogue PK(K2A2K2A)3K2AK3 with charge [+18]
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                                                                                                                                                                                                                                                                                                                                                                            29.9%; Score 79.5; DB 2; Length 29; 69.0%; Pred. No. 0.25; tive 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                7 KEKAYAKKAEKAAKKAEAKAYKAAEAKKK 35
                                                                                                                                                                                                                                                                                                                                                                                                                                               Andrews PC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                               Disclosure; Page 13; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW06698 standard; peptide; 29 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                     heparin anticoagulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UNMI ) UNIV MICHIGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-011697/01.
                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
les 20; Conserv
                                                                                                                                                                                                                                                                                                                                                     Sequence 29 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wakefield TW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9635444-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-MAY-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW06698;
                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Region
                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Protamine sulphate (also called n-protamine or salmine protamine) is a polycationic peptide derived from salmon sperm and is used to reverse he anticoagulation. One of the major components of salmine protamine is a 32 amino acid peptide having a total cationic charge of [+21], with arginine accounting for 67% of the total sequence and for all of the positive charge. Peptides of 20-40 amino acids with total cationic charge less than [+21] and which are able, at least partially, to reverse the effect of heparin and/or low molecular weight heparin anticoagulants are claimed. Specifically, the peptides are polycationic analogues of n-protamine where the positive charge on the amino acid sequence is reduced by selective replacement of positively charged arginine residues with an uncharged residue, so that total cationic charge is less than [+21]. The new peptides are used in vivo to reverse the effects of heparin; they
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   have the same anti-heparin activity as protamine but are less toxic (because of the reduced number of positive charges) and are relatively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       easy and inexpensive to prepare. The present sequence represents a specific example of a protamine-like peptide with a charge of [+18] whi has been found to reverse the anticoagulation effects of both standard and low molecular weight heparin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
Peptide reversing the anticoagulant effects of heparin - is based on protamine but has fewer positive charges for reduced toxicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           n-protamine; anticoagulation reversal; low molecular weight heparin; polycationic; positively charged amino acid; lysine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Length 29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "N-terminal is acetylated"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 79.5; DB
Pred. No. 0.25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 KEKAYAKKAEKAAKKAEAKAYKAAEAKKK 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                        Disclosure; Page 13; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR90178 standard; peptide; 29 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 29.9%;
1 Similarity 69.0%;
20; Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94WO-US012981
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 29 AA;
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cationic charge and lower toxicity, used for reversing (low mol.wt.) heparin anticoagulation.

Disclosure; Page 13; 34pp; English

Novel peptides are claimed which contain 20-40 amino acids and which have a total cationic charge of less than +21 (pref. +16 to +18; esp. +18) as determined by the number of positively charged amino acids in the sequence. Preferably the positive charges are grouped in clusters separated by neutral amino acids. Especially the peptides contain 28-32 amino acids having blocks of 2-4 positively charged amino acids separated by blocks of 2-6 neutral acids. Alternatively the positive charge may be distributed evenly or randomly along the peptide sequence. In particular the peptides are analogues of n-protamine (total cationic charge +21) in which selected arginine residues have been replaced by other positively charged amino acids and other arginine residues have been replaced by other positively charged amino acid residues, preferably lysine. The peptides amino acids and other arginine residues have been replaced by other positively charged amino acid residues, preferably lysine. The peptides chence can be used medically to prevent bleeding after the conclusion of clinical procedures using heparin therapy. They are less toxic than n-cordity ratio; and they may be more effective than n-protamine in their anti-LMMH action. The present sequence (total cationic charge = 16) is a specific example of the new polypeptides

Sequence 29 AA;

Gaps ; 0 Query Match 29.7%; Score 79; DB 2; Length 29; Best Local Similarity 67.9%; Pred. No. 0.28; Matches 19; Conservative 2; Mismatches 7; Indels Query Match

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Search completed: June 3, 2005, 10:37:08 Job time : 158 secs

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3, 2005, 10:37:19 ; Search time 137 Seconds (without alignments) 141.300 Million cell updates/sec
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(gnz 6/ptodata1/pubpaa/US10 NEW PUB.pep:*

(gnz 6/ptodata1/pubpaa/US10 NEW PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1465611 seqs, 345679903 residues
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                                                                                                                                                     OM protein - protein search, using sw model
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Sequence:

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Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES

	Description	Sequence 3, Appli	Sequence 3, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 17, Appl	Sequence 41, Appl	Sequence 177669,	Sequence 50521, A	Sequence 23, Appl	Sequence 182752,	Sequence 240336,
	αı	US-09-816-989A-3	US-10-792-311-3	US-09-816-989A-2	US-10-792-311-2	US-09-816-989A-1	US-10-792-311-1	US-10-667-004-17	US-10-229-567-41	US-10-424-599-177669	US-10-767-701-50521	US-10-667-004-23	US-10-424-599-182752	US-10-424-599-240336
	DB	6	17	σ	17	σ	17	16	14	15	16	16	15	15
	Query Match Length DB	95	26	45	45	35	35	49	55	55	53	26	51	53
de	Query Match	100.0	100.0	50.6	50.6	39.3	39.3	31.0	28.8	28.6	28.2	28.2	27.4	27.4
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15 US-10-424-599-247907 16 US-10-437-965-138732 15 US-10-424-599-216336 15 US-10-424-599-210306 19 US-09-805-301-128 19 US-09-805-301-139 19 US-10-424-599-18635 15 US-10-424-599-18635 15 US-10-424-599-18635 16 US-10-424-599-18635 17 US-10-424-599-18635 18 US-10-424-599-18635 19 US-10-424-599-18637 19 US-09-805-301-73	9 US-09-805-301-75 15 US-10-424-599-169296
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73 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	01 01
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ALIGNMENTS

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Sequence 3. Application US/09816989A

j Sequence 3. Application US/09816989A

general No. US20020115103A1

GENERAL INFORMATION:

APPLICANT: Gad, Alexander

APPLICANT: Gad, Alexander

TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKE

TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKE

TITLE OF INVENTION: COPOLYMER 1 US/09/816,989A

CURRENT FILING DATE: 2001-03-23

PRIOR PAPLICATION NUMBER: 60/101,693

PRIOR PLILING DATE: 1999-09-25

PRIOR PLILING DATE: 1999-09-25

PRIOR PLILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patentin version 3.1

SEQ ID NO 3

LENGTH: 56

MANDER APPLICATION NUMBER: PATENTIAL OF THE SEQ ID NOS: 7

LENGTH: 56
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 266; DB 9; ilarity 100.0%; Pred. No. 1.5e-18; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
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nes 56; Conservat
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Matches
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RESULT 2

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APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKE
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-USE
CURRENT APPLICATION NUMBER: US/10/792,311
CURRENT FILING DATE: 2004-03-02
PRIOR APPLICATION NUMBER: 06/101,693
PRIOR PILING DATE: 1999-09-25
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR PILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PARCHIN VERSION 3.1
SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKE
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR APPLICATION NUMBER: DCT/US99/22402
PRIOR APPLICATION NUMBER: DCT/US99/22402
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIAN DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: DATENTIAN DATE: LINE DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----KKAYKAAEAKK--AAKYEKAAAEKAAKEAAYEA
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Pred. No. 3.9e-06;
0; Mismatches 5; Indels 13
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Patent No. US200201151031A1
GENERAL INFORMATION:
APPLICANT: Gad, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
US-10-792-311-1
; Sequence 1, Application US/10792311
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51.8%;
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                     Publication No. US20050038233A1
GENERAL INFORMATION:
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Best Local Similarity 51.8°
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US-09-816-989A-1
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                                                                                                                                APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989
CURRENT FILING DATE: 2004-03-02
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR FILING DATE: 1998-09-25
PRIOR PELING DATE: 1998-09-25
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PALENTING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SEQ ID NO 3
LENGTH: 56
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TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT PAPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001.03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 7
SEQ THANKE: PATCHING DATE: 1999-09-34
NUMBER OF SEQ ID NOS: 7
SEQ ID NO 2
LENGTH: 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-10-792-311-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKY-KAEAAKAAAKEAAYEA 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 266; DB 17; Best Local Similarity 100.0%; Pred. No. 1.5e-18; Matches 56; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09816989A Patent No. US20020115103A1
                              Sequence 3, Application US/10792311
Publication No. US20050038233A1
GENERAL INFORMATION:
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APPLICANT: Gad, Alexander
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US-10-792-311-3
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US-10-792-311-2
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Solu Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE REFERENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 177669
LENGTH: 55
                                                                                                                                    Ulcerative Colitis, and Clinical Subtypes Thereof, Using Microbial UC pANCA antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7
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                                                                           Cohavy, Offer TITLE OF INVENTION: Diagnosis, Prevention and Treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/229,567
FILING DATE: 27-Aug-2002
CLASSIFTCATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/417,264
FILING DATE: «Unknown»
APPLICATION NUMBER: US 09/041,889
FILING DATE: «Unknown»
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 9-PM 3006
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 41:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 177669, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       535-8949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 55 amino acids
GENERAL INFORMATION:
APPLICANT: Braun, Jonathan
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                                                                                                                                                                                                                                                                                                                                                                  CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
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Matches 26; Conservative
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ORGANISM: Glycine max
PEATURE:
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                      GENERAL INFORMATION:
APPLICANT: dis, Obcis
TITLE OF INVENTION:
TITLE OF INVENTION:
AND FOR THERAPEUTIC USE
TITLE OF INVENTION:
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APPLICANT: INTEL CORPORATION
APPLICANT: CHAN, Selena
APPLICANT: CHAN, Selena
APPLICANT: CHAN, Selena
APPLICANT: SU, Xing
APPLICANT: VAMAKAWA, Mineo
TITLE OF INVENTION: CONTROLLED ALIGNMENT OF NANO-BARCODES ENCODING SPECIFIC INFORMATI
TITLE OF INVENTION: SCANNING PROBE MICROSCOPY (SPM)
FILE REFERENCE: INTEL1110-1(P14240X)
CURRENT PLING DATE: 2003-09-19
PRIOR APPLICATION NUMBER: US/10/667,004
PRIOR APPLICATION NUMBER: US 10/251,152
PRIOR APPLICATION NOS: 26
SOFTWARE: Patentin version 3.1
SEQ ID NO 17
LENGTH: 49
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Pred. No. 0.0021;
4; Mismatches 2; Indels 21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKYKAEAAKAAAKEAAYEA 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 41, Application US/10229567 Publication No. US20030092080A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17, Application US/10667004 Publication No. US20040126820A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 39.3%;
Best Local Similarity 51.8%;
Matches 29; Conservative '
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence FEATURE:
       Publication No. US20050038233A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-229-567-41
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Sequence 240336, Application US/10424599

Sequence 240336, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Boy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION NUMBER: US/10/424,599

CURRENT APPLICATION NUMBER: US/20/304-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 240336

LENGTH: 53
                                                                                                                                                                                                                                                                   APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yould K
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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        26
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                                                             2 KKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKYKAEAAKAAAKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 27.4%; Score 73; DB 15; Length 51; Best Local Similarity 42.2%; Pred. No. 3.2; Matches 19; Conservative 5; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 27.4%; Score 73; DB 15; Length 53; Best Local Similarity 38.0%; Pred. No. 3.3; Matches 19; Conservative 7; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 KKNYKKKKKKKKKKKKKKKKKKKKKKK 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , OTHER INFORMATION: Clone ID: PAT_MRT3847_136039C.1.pep
US-10-424-599-182752
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US-10-424-599-240336
                                                                                                                                                                                               ; Sequence 182752, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 247907, Application US/10424599
; Publication No. US20040031072A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Glycine max
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US-10-424-599-247907
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 182752
LENGTH: 51
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; Sequence 23, Application US/10667004
; Publication No. US20040126820A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: INTEL CORPORATION
APPLICANT: GLAN, Selena
APPLICANT: SU, Xing
APPLICANT: YAMAKAWA, Mineo
TITLE OF INVENTION: CONTROLLED ALIGNMENT OF NANO-BARCODES ENCODING SPECIFIC INFORMATI
TITLE OF INVENTION: SCANNING PROBE MICROSCOPY (SPM)
TITLE OF INVENTION: SCANNING PROBE MICROSCOPY (SPM)
TITLE OF INVENTION: SCANNING PROBE MICROSCOPY (SPM)
CURRENT PELLING DATE: 2003-09-19
PRIOR APPLICATION NUMBER: US 10/251,152
PRIOR APPLICATION NUMBER: US 10/251,152
NUMBER OF SEQ ID NOS: 26
NUMBER OF SEQ ID NOS: 26
NUMBER PATELLING DATE: 2002-09-20
NUMBER: PATELLING DATE: 2002-09-20
NUMBER PATELLING DATE: 2002-09-20
NUMBER PATELLING DATE: 2003-09-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 50521
LENGTH: 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 28.2%; Score 75; DB 16; Length 56; Best Local Similarity 48.1%; Pred. No. 2.2; Matches 25; Conservative 1; Mismatches 26; Indels
                                                                                                                                                                                                                                     2 KKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKYKAEAAK 46
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                                                                                                                                                Indels
; OTHER INFORMATION: Clone ID: PAT_MRT3847_131450C.1.pep
US-10-424-599-177669
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US-10-767-701-50521
                                                                                                                                                20;
                                                                      zuciy match
Best Local Similarity 40.0%; Pred. No. 1.8;
Matches 18; Conservative 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 50521, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
APPLICANT: KOYALIC, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:

OTHER INFORMATION: Synthetic peptide
US-10-667-004-23
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Best Local Similarity 42.2'
Matches 19; Conservative
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LENGTH: 56
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APPLICANT: LA ROALISM:
APPLICANT: LA ROALISM:
APPLICANT: Exountic, David K.
APPLICANT: Shou, Yihua
APPLICANT: Shou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Bridge Mither and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERBYCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 138732
LENGTH: 54
       APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Abou Vihua
APPLICANT: Zhou Vihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 247907
LENGTH: 53
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27.4%; Score 73; DB 15; Length 53;
Best Local Similarity 45.0%; Pred. No. 3.3;
Matches 18; Conservative 4; Mismatches 18; Indels
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US-10-424-599-247907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 KKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKYK 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: PAT_MRT4530_40093C.1.pep
US-10-437-963-138732
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13872, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
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Best Local Similarity 45.0°
Matches 18; Conservative
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Glycine max PEATURE:
GENERAL INFORMATION:
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US-10-437-963-138732
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Search completed: June 3, 2005, 10:50:08 Job time: 138 secs

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June 3, 2005, 10:29:08 ; Search time 42 Seconds (without alignments) 99.532 Million cell updates/sec
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2: /cgn2 6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2 6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2 6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2 6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-816-989A-1
US-09-816-989A-1
US-09-816-989A-1
US-08-93-008A-6
US-08-193-008A-5
US-08-193-008A-5
US-08-193-008A-5
US-08-303-025-15
US-08-303-025-14
US-08-303-025-14
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US-08-303-025-14
US-08-303-025-14
US-08-303-025-14
US-08-303-025-10
US-08-303-025-10
US-08-303-025-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            513545 seqs, 74649064 residues
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Listing first 45 summaries
                                                                                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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266
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Maximum DB seq length: 56
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Sequence 41, Appl	Sequence 41, Appl	Sequence 12, Appl	Sequence 1, Appli	Sequence 29, Appl		Sequence 29, Appl		٠	٠	Sequence 29, Appl	Sequence 29, Appl	Sequence 29, Appl					
US-09-041-889-41	US-09-417-264-41	US-08-303-025-12	US-08-436-703B-1	US-08-231-730A-29	US-08-427-001C-29	US-08-457-798-29	US-08-457-171-29	US-08-505-486-29	US-08-689-489C-29	US-08-801-028-29	US-09-340-154-29	US-09-232-802A-29	US-09-482-611B-29	US-09-019-922A-29	PCT-US94-06176-29	PCT-US94-12550-29	PCT-US95-04335-29
55 3	55 4	28 1	28 2	37 1	37 1	37 1	37 1	37 2	37 3	37 3	37 3	37 3	37 4	37 4	37 5	37 5	37 5
76.5 28.8	76.5 28.8	74 27.8	74 27.8					74 27.8		74 27.8	74 27.8		74 27.8		74 27.8	74 27.8	74 27.8
28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A
FILE REFERENCE: 60807-A
CURRENT PPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1 sequence 3, Application US/09405743A; Patent No. 6514938; GENERAL INFORMATION: TYPE: PRT ORGANISM: Artificial Sequence US-09-405-743A-3 SEQ ID NO 3 LENGTH: 56 FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: PEPTIDE US-09-405-743A-3

Query Match 100.0%; Score 266; DB 4; Length 56; Best Local Similarity 100.0%; Pred. No. 3.2e-20;

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Gaps

0; Indels

0; Mismatches

56; Conservative

US-V=10-7 SEP-7594-3.

US-Gquence 3, Application US/09816989A

Patent No. 6800287

GENERAL INFORMATION:

APPLICANT: Gis, Doris

TITLE OF INVENTION:

PILE REFERENCE: 2609/60807-A-PCT-US

CURRENT PILING DATE: 2001-03-23

PRIOR PILING DATE: 1999-09-25

PRIOR PILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 7

SOFTWARE PILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 7

SOFTWARE PILING DATE: 1999-09-34

SOFTWARE PILING DATE: 1999-09-34 US-09-816-989A-3 음

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39; Conservative
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LENGTH: 35
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TITLE OF INVENTION: AND FOR THERAPEUTIC USE
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
TILE REPERENCE: 2609/60807—A-ECT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR PILING DATE: 1998-09-25
PRIOR FILING DATE: 1999-09-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.
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                                                      OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKY-KAEAAKAAKEAAYEA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                       13; Gaps
                                                                                                                                                                                               1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAEAKYKAEAAKAAAKEAAYEA 56
                                                                                                                                                                                                                                                                                                      TITLE OF INVESTIGNT: Yeda Research and Development Co., Ltd.
TITLE REPERENCE: 60807-A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 45
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYNTHETIC
                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.6%; Score 134.5; DB 4; Length 45; 68.4%; Pred. No. 3.5e-07;
                                                                                                               Length 56;
                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: PEPTIDE
                                                                                                             Query Match
100.0%; Score 266; DB 4;
Best Local Similarity 100.0%; Pred. No. 3.2e-20;
Matches 56; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50.6%; Score 134.5; DB 4 68.4%; Pred. No. 3.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09816989A Patent No. 6800287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 45
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 68.44 Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                             US-09-816-989A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-405-743A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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TITLE OF INVENTION: COPOLYMER I RELATED POLYBEPTIDES FOR USE AS MOLECULAR WEIGHT MARKE TITLE OF INVENTION: AND FOR THERAPEUTIC USE RILE REFERENCE: 2609/60807-a-PCT-US CURRENT APPLICATION NUMBER: US/09/816,989A CURRENT FILING DATE: 2001-03-23 PRIOR APPLICATION NUMBER: 60/101,693 PRIOR FILING DATE: 1998-09-25 PRIOR FILING DATE: 1998-09-25 PRIOR FILING DATE: 1998-09-25 PRIOR FILING DATE: 1999-09-24 NUMBER: OF SEQ ID NOS: 7 SOFTWARE: PATCHIN Version 3.1
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7
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
                                                                                            Gaps
13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----EAKAKAAEAAKEAAYEA 35
                                               1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAABAKKKAEAKY-KAEAAKAAAKEAAYEA
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                                                                                                                                                                                                                                                                   APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GLAFIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT PILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 104.5; DB 4; Length 35;
Pred. No. 0.00027;
4; Mismatches 2; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 104.5; DB 4; Length 35;
Pred. No. 0.00027;
4; Mismatches 2; Indels 2
  5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: PEPTIDE
US-09-405-743A-1
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
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                                                                                                                                                                                                                    ; Sequence 1, Application US/09405743A; Patent No. 6514938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09816989A Patent No. 6800287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 39.3%;
1 Similarity 51.8%;
29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
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1 Similarity 51.8%;
29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Gad, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 29; Conserv
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4; Mismatches
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PRIOR APPLICATION DATA:
PAPLICATION NUMBER: 9CT/US92/08069
FILING DATE: 14-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SS: not relevant not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 303-499-8089
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28; Conservative
                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 28; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: no
MOLECULE TYPE:
                                           80303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-993-008A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-152-488-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39.1%; Score 104; DB 3; Length 56; 58.2%; Pred. No. 0.00049; tive 4; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/993,008A
FILING DATE: 18-DEC-1997
CLASSIFICATION: 514
FRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/032,436
FILING DATE: 18-DEC-1996
ATTORNEY AGENT INFORMATION:

NAME: Sullivan, Sally A.

REFERENCE/DOCKET NUMBER: 33-95
TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFHONE: 303-499-8080
                                                                        APPLICANT: Liotta, Dennis C.
APPLICANT: Petros, John A.
APPLICANT: Wey, Shiow-Jyi
APPLICANT: Warr, Joan F.
APPLICANT: Karr, Joan F.
APPLICANT: Karr, Joan F.
APPLICANT: SCHOOL, Jan
TITLE OF INVENTION: Polycationic Oligomers
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan
STREET: 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Liotta, Dennis C.
APPLICANT: Liotta, John A.
APPLICANT: Wey, Shiow-Jyi
APPLICANT: Karr, Joan F.
APPLICANT: Poll, Jan
TITLE OF INVENTION: Polycationic Oligomers
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                  Sequence 6, Application US/08993008A Patent No. 6153596
GENERAL INFORMATION:
APPLICANT: Liotta, Dennis C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/08993008A Patent No. 6153596
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not relevant
E: peptide
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TELEFAX: 303-499-8089
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39.1%
Best Local Similarity 58.2%
Matches 32, Conservative
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LENGTH: 56 amino acids
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , ANTI-SENSE: NO
US-08-993-008A-6
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US-08-993-008A-6
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37.4%; Score 99.5; DB 3; Length 48; 58.3%; Pred. No. 0.0012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 13, Application US/08152488
Patent No. 5534619
GENERAL INFORMATION:
APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN AND TITLE OF INVENTION: ANTICOAGULATION REVERSAL
NUMBER OF SEQUENCES:
ADDRESSEE: Benita J. Rohm, Esq.
COMPUTER REALDER FORM
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,008A
FLING DATE: 18-DEC-1997
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATE: 06/032,436
FLING DATE: 18-DEC-1996
ATPOINTS NUMBER: US 60/032,436
FILING DATE: 18-DEC-1996
ATPOINTS NUMBER: 32,064
REGISTRATION NUMBER: 32,064
REGISTRATION NUMBER: 33,95
TELEPHONE: 303.499.6080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: 512 Springfield Avenue
STREET: 512 Springfield Avenue
CITY: Cranford
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07016-1811
COMPUTER: ELADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS
SOFFWARE: Wordberfect 6; ASCII (DOS) Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/152,488
FILING DATE: 12-NOV-1993
CLASSIFICATION: 514
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Query Match
31.6%; Score 84; DB 1; Length 32;
Best Local Similarity 62.9%; Pred. No. 0.028;
Matches 22; Conservative 3; Mismatches 6; Indels
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Patent No. 5721212

GENERAL INFORMATION:
APPLICANT: Wakefield, Thomas W.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN TITLE OF INVENTION: ANTICOAGULATION REVERSAL NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSE: Benita J, Rohm, Esq.
STREET: 512 Springfield Avenue
CITY: Cranford
STATE: New Jersey
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                    2 AKKAAKKAKKAKKAKKAAKKAK----KAAKKAKK 32
                                                                                                                                                                                                                                                                                                                                                                                                          1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKK 35
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordberfect 6; ASCII (DOS) Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/677,304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/152,488
FILING DATE: 12-NOV-1993
APPLICATION NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: ROAM, Benita J.
RESISTRATION NUMBER: 28,664
REFERENCE/DOCKET NUMBER: RA-7WG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: No. 5721212 Relevant
TOPOLOGY: No. 5721212 Relevant
                                                                                                                                                                                                            TITLE: N/A
DOCUMENT NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-276-3344
                        32 amino acids
  SEQUENCE CHARACTERISTICS
                                                                                                                                        ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    908-276-5543
                                                                                 TOPOLOGY: N/A
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                         TYPE: amino acid
STRANDEDNESS: N/
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US-08-677-304-13
                                                                                                                                                                                                                                                                               US-08-303-025-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Andrews, Philip C.
APPLICANT: ACANLEWS, Philip C.
APPLICANT: ACANLEWS, PRINCE C.
APPLICANT: ALSO FOR HEPARIN AND TITLE OF INVENTION: NOWEL PEPTIDES FOR HEPARIN TITLE OF INVENTION: ANTICOAGULATION REVERSAL NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE Benita J, Rohm, Esq.
STREET: 150 West Jefferson, Suite 2500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKK 35
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               NAME: Rohm, Benita J.
REGISTRATION NUMBER: 28,664
RESTENENCE/DOCKET NUMBER: RM-7WG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-276-3344
TELEFAX: 908-276-5543
INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                   PUBLICATION INFORMATION:
COCUMENT NUMBER: PCT/US92/08069
CLING DATE: 14-AUG-1993
US-08-152-488-13
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; Sequence 15, Application US/08303025
; Patent No. 5614494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 313-496-7622
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: N/A
TOPOLOGY: N/A
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 313-496-8454 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                    ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
                                                                                                                                                                                                                                                                                                                                                                                    N/A
                                                                                                                                                                                                                                                                                                                                                              AUTHORS:
TITLE: N
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Gaps 4

6; Indels

62.9%; Pred. No. 0.028; tive 3; Mismatches

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2 AKKAAKKAAKKAKKAKKAK----KAAKKAKK 32
                                               1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKK 35
Best Local Similarity 62.9
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S:
Matches 22
                                                                                                                                RESULT 13
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                                                                                                                                                               Gaps
                                                                                                                                                               4;
                                                                                                                           Query Match 31.6%; Score 84; DB 1; Length 32; Best Local Similarity 62.9%; Pred. No. 0.028; Matches 22; Conservative 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                            Sequence 2. Application US/08436703B
Patent No. 5919761
Patent No. 5919761
Patent No. 5919761

Paperlicant wheefield, Thomas W. APPLICANT Andrews, Philip C. APPLICANT Stanley, James C. TITLE OF INVENTION: HEPARIN AND LOW MOLECULAR; TITLE OF INVENTION: WEIGHT HEPARIN TITLE OF INVENTION: WEIGHT HEPARIN TITLE OF INVENTION: WEIGHT HEPARIN TITLE OF INVENTION: ANTICOAGULATION REVERSE CORRESPONDENCE ADDRESSE: BE CORRESPONDENCE ADDRESSE: Benita J, Rohm, Esq. STREET: 6601 Woodward Avenue
                                                                                                                                                                                                             2 AKKAAKKAAKKAAKKAAKKAK 32
                                                                                                                                                                                           1 AKKYAKKEKAYAKKAEKAAKKARAKAYKAAEAKKK 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Michigan
COUNTRY: United States of America
                                                PUBLICATION INFORMATION:
DOCUMENT NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 313-965-1951
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PUBLICATION INFORMATION:
AUTHORS: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
TITLE: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: N/A
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Detroit
STATE: Michia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-436-703B-2
                                                                                                US-08-677-304-13
                                                                                                                                                                                                                                                                                    -08-436-703B-2
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                                                                                                  APPLICANT: Wakefield, Thomas W.
APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: NOVEL PEPTIDES FOR HEPARIN AND TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN TITLE OF INVENTION: ANTICOAGULATION REVERSAL NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benita J. Rohm, Esq.
                                                                                                                                                                                                                                                                                                                                                                 CITY. Detroit States of America STATE: Michigan COUNTRY: United States of America ZIP: Wichigan CONFUTER: United States of America ZIP: Wichigan COMPUTER READABLE FORM: MS-DOS V. 6.22 CONFUTER: Floppy diskette 3.5" 1.44Mb COMPUTER: HBM PC COMPATIBLE MS-DOS V. 6.22 SOFTWARE: WordPerfect 6.1; ASCII (DOS) Text CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/303,025 FLING DATE: 08-SEPT-1994 CLASSIFICATION NUMBER: US/08/20/06829 FLING DATE: 14-AUG-1992 APPLICATION NUMBER: US/08/152,488 FLING DATE: 14-AUG-1993 ATTORNEY/AGENT INFORMATION: NAME: Rohm, Benita J. REPERRENCE/DOCKET NUMBER: 7WH-060548-00231 TELECHONE: 313-496-7622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAABAKKK 35
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                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Benita J, Rohm, Esq.
STREET: 150 West Jefferson, Suite 2500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE: N/A
DOCUMENT NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
US-08-303-025-16
; Sequence 16, Application US/08303025
; Patent No. 5614494
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: N/A MOLECULE TYPE: PORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-303-025-16
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RESULT 14

Length 32;

DB 2;

31.6%; Score 84;

Query Match

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TITLE OF INVENTION: ANTICOAGULATION REVERSAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 84; DB 2; Length 33;
Pred. No. 0.029;
3; Mismatches 6; Indel8
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Sequence 12, Application US/08152488

Patent No. 5534610:

APPLICANT: Wakefield, Thomas W.

APPLICANT: Andrews, Philip C.

APPLICANT: Stanley, James C.

TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN AND TITLE OF INVENTION: LOW MOLECULAR WEIGHT HEPARIN
                                                                                                APPLICANT: Wakefield, Thomas W.
APPLICANT: Andrews, Philip C.
APPLICANT: Andrews, Philip C.
APPLICANT: Stanley, James C.
TITLE OF INVENTION: HEPATIN AND LOW MOLECULAR TITLE OF INVENTION: WEIGHT HEPATIN TITLE OF INVENTION: WIGHT HEPATIN NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS: Benita J, Rohm, Esq.
STREET: 6601 Woodward Avenue
STREET: Suite 1525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKK 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: MS-LOJS
SOFTWARE: WordPerfect 6;
SOFTWARE: WordPerfect 6;
SOFTWARE: ASCII (DOS)Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,703B
FILING DATE: 08-MAY.1995
CLASSIFICATION: 5.14
PRIOR APPLICATION DATA:
APPLICATION NUMBER: N/A
FILING DATE: N/A
ATTORNEY/AGENT INFORMATION:
NAME: ROPM: ABROIT A.
REGISTRATION NUMBER: 28,664
REFERENCE/DOCKET NUMBER: 28,664
REFERENCE/DOCKET NUMBER: 7WK-060548-
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 4826
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk 1.44Mb, 3.5"
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Detroit
STATE: Michigan
COUNTRY: United States of America
                       Sequence 4, Application US/08436703B
Patent No. 5919761
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 62.9%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: N/A
FOPOLOGY: N/A
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
TITLE: N/A
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Gaps
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                                                                CITY: Cranford
STATE: New Jersey
COUNTY: United States of America
ZIP: 07016-1811
COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6; ASCII (DOS)Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/152,488
FILING DATE: 12-NOV-1993
CLASSIFICATION: 514
PRIOR APPLICATION INFORMATION:
APPLICATION NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
ATTORNEY, AGENT INFORMATION:
NAME: ROAM: Benita J:
REGISTRATION NUMBER: 28,664
REFERENCE/DOCKET NUMBER: RM-7WG
TELEPHONE: 908-276-53434
TELEPHONE: 908-276-5543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 KEKAYAKKAEKAAKKAEAKAYKAAEAKKK 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 KKKA-AKKAKKAKKAKKAKKKK 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PUBLICATION INFORMATION:
DOCUMENT NUMBER: PCT/US92/08069
FILING DATE: 14-AUG-1993
CORRESPONDENCE ADDRESS:
ADDRESSEE: Benita J, Rohm, Esq.
STREET: 512 Springfield Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: N/A
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: N/A
PUBLICATION INFORMATION:
AUTHORS: N/A
TITLE: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: N/
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version	- 2005
enCore	1993
g	ΰ
	Copyright

OM protein - protein search, using sw model

June Run on:

3, 2005, 10:46:55 ; Search time 38 Seconds
(without alignments)
167.113 Million cell updates/sec

Title: Perfect score:

US-10-792-311-4 313 1 AKKYAKKEKAYAKKAEAK......BAKYKAEAAKAAAKEAAYEA 66 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

18903 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 66

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

PIR_79:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d			SUMMARIES	
Result No.	Score	& Query Match	g Query Match Length	08	ΙD	Description
-	79	25.2	62	~	T30977	hypothetical prote
7	68.5	21.9	45	~	S10544	•-
m	68.5	21.9	45	~	S04941	
4	68.5	21.9	45		S10545	protamine phi-3.3
S	9	19.2			A87439	hypothetical prote
9	26	17.9	45		A05163	antifreeze protein
7	55.5	17.7	44	~	PT0028	tandem repeat pept
60	55	17.6	63	~	F83293	
0,	52.5	16.8	99	~	163131	metallothionein ol
10	51.5	16.5	99	7	A86729	mercuric reductase
11	51	16.3	51	7	AS6371	collagen alpha 1(X
12	50.5	16.1	. 62	7	H64443	hypothetical prote
13	50.5	16.1	65		A95330	hypothetical prote
14	20	16.0	40	-	FDF18G	antifreeze protein
15	49.5	15.8	64		S70831	ribosomal protein
16	49	15.7	26		T09177	ydaE protein - Esc
17	49	15.7	61		A64163 .	ribosomal protein
18	49		64		H86286	hypothetical prote
19	48.5				B40186	ubiquitin / riboso
20	48.5	15.5		•	S78292	ribosomal protein
21	48.5	15.5		•	S78240	ribosomal protein
22					AD3327	hypothetical prote
23	48	•			S77143	al
24	48	15.3			T07317	υ
25	48	٠			S73128	
56	48	15.3			S60851	M protein precurso
27	48	15.3	62	~	F69532	
28	4	15.3	64		T13381	hypothetical prote
53	47.5	15.2	57	~	A82778	

Distribute phi-3.2 - California mussel
N.Alternate names: protamine PL-TV.2
C,Species: Mytilus californianus (California mussel)
C,Species: Mytilus californianus (California mussel)
C,Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C,Accession: S10644
R,Ausio, J.; McParland, R.
Eur. J. Biochem. 182, 569-576, 1989
A,Title: Sequence and characterization of the sperm-specific protein phi3 from Mytilus C&A,Reference number: S04941; MuID:89325302; PMID:2666130

A,Molecule type: protein A,Residues: 1-45 AAUS> A,Cross-references UNIPROT:P11860 C,Superfamily: histone H1 C,Keywords: DNA binding; nucleus

hypothetical prote gene 14 protein - B. subtilis YwmG p	B. subtilis YwmG p human 4F5S homolog myosin heavy chain	hypothetical cytos antifreeze protein	myosin catalytic l histone Hl.a, hepa	M-11Ke protein pre hypothetical prote ribosomal protein	sperm-specific pro homeotic protein u hypothetical prote
G89944 S58143 AF1344	A11714 T38070 S61536	AB3394 FDFISG	S01945 S24179	S62076 I40892 H71666	B45316 S58853 AD1413
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48 58 61	63	33 22	5.4	0 0 0 0 0 0 0 0 0	35 40 51
15.0	15.0	15.0	14.7	14.7 14.7 14.7	14.5 14.5 14.5
74 74 74	444	44	4 4 6 6 6 6	4 4 4 0 0 0	45 5.5 5.5 5.5
30 31	ነ ርህ ይህ ሲ በ ርህ 44 ቢ	36	866	4 4 4 0 1 2	4 4 4 5 4 5

ALIGNMENTS

hypothetical protein CO1B10.5 - Caenorhabditis elegans C;Species Caenorhabditis elegans C;Species Caenorhabditis elegans C;Species Caenorhabditis elegans C;Accession: T30977 R;Blanchard, M; Bradshaw, H. submitted to the EMBL Data Library, August 1999 A;Reference number: 220949 A;Reference mumber: 22044 A;Re	RESULT 1 T30977	
09-Jul-2004 6; Gaps KAEAKAARK 60 : KSPAKKAAPK 60	hypothetical protein C01B10.5 - Caenorhabditis elegan C.Speries. Caenorhabditis elegans	5 0
6; Gaps KAEAKAAAK 60 : KSPAKKAAPK 60	C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #t	ext_change 09-Jul-2004
6; Gaps KAEAKAAAK 60 : KSPAKKAAPK 60	C;Accession: T30977	ı
6; Gaps KAEAKAAAK 60 : KSPAKKAAPK 60	K;Bianchard, M.; Bradshaw, H. gubmitted to the EMBL Data Library, August 1999	
6; Gaps KAEAKAARK 60 : KSPAKKAAPK 60	A; Description: The sequence of C. elegans cosmid C01B	10
6; Gaps KAEAKAAAK 60 : KSPAKKAAPK 60	A; Kelerence number: 220949 A: Accession: T30977	
6; Gaps Kaearkaark 60 : KSPAKKAAPK 60	A;Status: preliminary; translated from GB/EMBL/DDBJ	
6; Gaps Kaearkaark 60 : KSPAKKAAPK 60	A; Molecule type: DNA	
79; DB 2; Length 62; No. 4; matches 21; Indels 6; Gaps AEAKKYAKAAKAEKKEYAAAEAKYKAEAAKAAAK 60 AEAKKYAKAAKAEKKEYAAAEAKYKAEAAKAAAK 60 ASPKK-AAAPKA-KKPVKKAAAK-KSPAKKAAPK 60	A; Cross-references: UNIPROT:Q17536; EMBL:U58757; PIDN	:AAC47916.1
17	A, Experimental source: strain Bristol N2	
61/3 25.2%; Score 79; DB 2; Length 62; Conservative 4; Mismatches 21; Indels 6; Gaps CYAKKEKAYAKKAEAKKAKAEAKKYAKAAAKKAAAKKAEAKAAAK 60 CYAKTKKVAAKPKAPKVKKIQASPKK-AAAPKA-KKPVKKAAAK-KSPAKKAAPK 60 11	C;Genetics:	
25.2%; Score 79; DB 2; Length 62; Conservative 4; Mismatches 21; Indels 6; Gaps CYAKKEKAYAKKAEAKKAKAEAKKYAKAAAKEKEYAAAEAKYYAEAAKAAAK 60 CYAKTKKVAAKPKAPKVKKIQASPKK-AAAPKA-KKPVKKAAAK-KSPAKKAAPK 60		
Duery Match 25.2%; Score 79; DB 2; Length 62; Sest Local Similarity 49.2%; Pred. No. 4; datches 30; Conservative 4; Mismatches 21; Indels 6; Gaps 1 AKKYAKKEKAYAKARAKAAKAAKAAKAAAKAAKAAAAKAA	A;Note: C01B10.5	
dest Local Similarity 49.2%; Pred. No. 4; 4atches 30; Conservative 4; Mismatches 21; Indels 6; Gaps 1 AKKYAKKEKAYAKKAEAKAKAEAKKYAKARAKKEYAKAAEKKEYAABAKYKAEAAKAAK 60 1 AKKYAKKKYAAKPKAPKYKKIQASPKK-AAAPKA-KKPYKKAAAK-KSPAKKAAPK 60 61 E 61 1 K 61	25.2%; Score 79; DB 2;	ength 62;
1 AKKYAKKEKAYAKAKKAEAKAAKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKAAKK	49.2%; Pred. No. 4; vative 4; Mismatches	Indels 6; Gaps
	н	
. 61 B	7	
: 61 K	. 61 B	
	: 61 K	
	S10544	

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Query Match
Best Local Similarity
Matches 16; Conserv
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A;Molecule type: mRNA
A;Residues: 1-44 <WAS>
                                                                                                                               A; Molecule type: DNA A; Residues: 1-58 <STO>
                                                                                                      A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: A05163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
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R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laud, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, J. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Vencer, J.C.; Fraser, C.M.
                                                                                                                                                                                                                                                                                                       N;Alternate names: protamine PL-IV.1.
C;Species: Mytilus californianus (California mussel)
C;Species: Mytilus californianus (California mussel)
C;Date: O'-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: S04941
R;Ausio, J.; McParland, R.
R;Ausio, J.; McParland, R.
A;Title: Sequence and characterization of the sperm-specific protein phi3 from Mytilus
A;Reference number: S04941; MUID:89325302; PMID:2666130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: S10545
R;Ausio, J.; McParland, R.
Eur. J. Biochem. 182, 569-576, 1989
A;Title: Sequence and characterization of the sperm-specific protein phi3 from Mytilus A;Reference number: S04941; MUID:89325302; PMID:2666130
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C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N;Alternate names: protamine PL-IV.3
C;Species: Mytilus californianus (California mussel)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
                                                       Gaps
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                                                                                                      12 AKAKKAEAKAAKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKAAAKE
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Query Match 21.9%; Score 68.5; DB 2; Length 45; Best Local Similarity 40.0%; Pred. No. 20; Matches 20; Conservative 6; Mismatches 19; Indels
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Best Local Similarity 40.0%; Pred. No. 20;
Matches 20; Conservative 6; Mismatches
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A;Note: 6-Thr, 17-Thr, and 18-Thr was also found
C;Superfamily: histone H1
C;Keywords: DNA binding; nucleus
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C;Superfamily: histone H1
C;Keywords: DNA binding; nucleus
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A,Molecule type: protein
A,Residues: 1-45 <AUS>
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Matches 20; Conserv
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R;Wallis, A.E.; McMaster, W.R.
J. Exp. Med. 166, 1814-1824, 1987
A;Title: Identification of Leishmania genes encoding proteins containing tandemly repeati
A;Reference number: PT0027; MUID:88061089; PMID:3502718
                                                                                                                                                                                                                  A,Cross-references: UNIPROT:09A834; GB:AE005673; NID:g13422913; PIDN:AAK23509.1; GSPDB:GR
C,Genetics:
A,Gene: CC1530
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C;Species: Myoxocephalus scorpius (shorthorn sculpin, daddy sculpin)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
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C;Species: Leishmania major
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: PT0028
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R; Hew, C.L.; Joshi, S.; Wang, N.C.; Kao, M.H.; Ananthanarayanan, V.: Bur. J. Biochem. 151, 167-172, 1985
A; Fitle: Structures of shorthorn sculpin antifreeze polypeptides. A; Reference number: A91150; MUID:85285003; PMID:4029130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 44;
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                                                                                                                                                                                                                                                                                                                                             Length 58
                                        crescentus.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescent
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: A87439
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9 QARKAKAKADDKARATENRVRFGRSKAEKSLÆAARAEK 46
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Best Local Similarity 47.2%; Pred. No. 1.9e+02;
Matches 17; Conservative 3; Mismatches 16;
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                                                                                                                                                                                                                                                                                                                                      Score 60; DB 2; 1
Pred. No. 1.1e+02;
8; Mismatches 4;
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C;Superfamily: antifreeze protein
C;Keywords: antifreeze; blocked amino end; plasma
F;9-45/Region: alanine-rich
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A;Experimental source: strain NIH S
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                                                                                                                                                                                                                                                                                                                                                                                                           16; Conservative
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A;Residues: 1-45 <HEW>
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collagen alpha 1(XI) chain, alternative exon 2b - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: A56371
R;Zhidkova, N.I.; Justice, S.K.; Mayne, R.
J. Biol. Cham. 270, 9486-9493, 1995
A;Fitle: Alternative mRNA processing occurs in the variable region of the pro-alpha 1(XI)
A;Reference number: A56371; MUID:95238468; PMID:7721876
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A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C. A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C. A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii. A;Reference number: A64300; MUID: 96337999; PMID: 8688087
C;Superfamily: mercuric resistance operon regulatory protein; heavy-metal-associated home
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: H64443
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                                                           Score 51.5; DB 2; Length (
Pred. No. 5.7e+02;
3; Mismatches 16; Indels
                                                                                                                                                                                                                               30 EKAKVSLKKNEALV------KFSAPADMDKMAVAVAEAGYK 64
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A;Molecule type: DNA
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                                                                 Query Match
Best Local Similarity 36.4%;
Matches 16; Conservative
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                                                                                                                                                                                              M.J.; Br
K.; Lim,
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A;Residues: 1-66 <STO>
A;Cross-references: UNIPROT:Q9CHA5; GB:AE005176; PID:g12723757; PIDN:AAK04931.1; GSPDB:G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fittle: The complete genome sequence of the lactic acid bacterium Lactococcus lactis se
Reference number: A86625, MUID:21235186, PMID:11337471
Accession: A86729
                                                                                                                                                                                                                                                                                                                    A,Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathd
A,Reference number: A82950; MUID:20437337; PMID:10984043
A,Accession: F83293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:Q91035; GB:AE004708; GB:AE004091; NID:g9948890; PIDN:AAG061:
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ribuguid, J.R.; Bohmont, C.W.; Liu, N.G.; Tourtellotte, W.W.
Proc. Natl. Acad. Sci. U.S.A. 86, 7260-7264, 1989
A;Title: Changes in brain gene expression shared by scrapie and Alzheimer disease.
A;Reference number: 148174; MUID:89386721; PMID:2780570
                                                                              C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: F83293
R;Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, J. Lory, S.; Olson, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mercuric reductase [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar_2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
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                                                                 lypothetical protein PA2808 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      metallothionein old gene name 'MT2' - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 31-May_1996 #sequence_revision 31-May-1996 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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16.8%; Score 52.5; DB 2; Length 66;
Best Local Similarity 40.9%; Pred. No. 4.7e+02;
Matches 18; Conservative 5; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.6%; Score 55; DB 2; Ilarity 42.9%; Pred. No. 2.9e+02; Conservative 7; Mismatches 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :::|:||| | :| || |:| |||:
ERMQAQAAKARAHQEKLAKQAEATKKD 59
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ses 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-63 <STO>
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A; Residues: 1-66 < RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: PA2808
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1;

Gaps

2,

Length 64; 24; Indels

Score 49.5; DB 2; Pred. No. 7.9e+02;

A; Accession: S70831

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A;Status: nucleic acid sequence not shown
A;Status: nucleic acid sequence not shown
A;Ratus: nucleic acid
A;Molecule type: DNA
A;Rasidues: 1-64 < CDAV>
A;Cross-references: UNIPROT:P49225; EMBL:U20669; NID:g710339; PIDN:AAB60205.1; PID:g71034
A;Genetics:
A;Genetics:
A;Genetics:
C;Superfamily: Escherichia coli ribosomal protein S21
C;Superfamily: becherichia coli ribosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Mismatches
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32.1%;
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Best Local Similarity 32.1
Matches 18; Conservative
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Job time : 40 secs
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A; Experimental source: strain 1021, megaplasmid pSymA
B; Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; Cience 293, 668-672, 2001
A; Hyman, R.W.; Jones, T.
A; Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner S.; Wells, D.H.; Wong, K.; Yeh, K. A; Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A; Contents: annotation
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C;Species: Myxococcus xanthus
C;Species: Myxococcus xanthus
C;Species: Myxococcus xanthus
C;Accession: S70831
R;Davis, J.M.; Mayor, J.; Plamann, L.
R;Davis, J.M.; Mayor, J.; Plamann, L.
A;Title: A missense mutation in rpoD results in an A-signalling defect in Myxococcus xan A;Reference number: S70829; MUID:96422481; PMID:8825098
                                                                                                     R.Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowe F. Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C. Pecc, Natl. Acad. Sci. U.S.A. 98, 9889, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot A;Reference number: A95262; MUID:21396509; PMID:11481432
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A;Title: Primary structures of the alanine-rich antifreeze polypeptides from grubby scul A;Reference number: 806417
A;Accession: 807046
A;Molecule type: protein
A;Residues: 1-40 <CHA>
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C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
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C;Species: Myoxocephalus aenaeus (grubby sculpin)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: S07046
R;Chakrabartty, A.; Hew, C.L.; Shears, M.; Fletcher, G.
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C,Superfamily: antifreeze protein
C,Keywords: antifreeze; blocked amino end
F;I/Modified site: blocked amino end (Met) #status experimental
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A;Molecule type: DNA
A;Residues: 1-65 <KUR>
                                                                       Accession: A95330
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A,Gene: SMa1009
A,Genome: plasmid
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EMBL; U58757; AAK66021.1; -. WormBase; WBGene00001858; hil-7.
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streptomyce
bdellovibri
mytilus cal
lactobacill
coxiella bu
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oryza sativ
leishmania
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trypanosoma
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bradyrhizob
arabidopsis
caulobacter
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plasmodium
homo sapien
streptomyce
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ashbya goss
streptococc
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candida gla
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caenorhabdi
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Q95qz0 caenorhabdi
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196.496 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                   1612378 seqs, 512079187 residues
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06S3G8
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073FW2
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09A834
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Q9SQZO
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Q9NFJ3
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Match Length DB
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Q99xv5 streptococc Q7cmq8 streptococc P04368 myoxocephal Q82py3 streptomyce Q8e6g8 streptococc Q8e0v1 streptococc Q9i035 pseudomonas Q7iip1 lactobacill Q74cw2 geobacter s Q86956 maize dwarf Q8jkj3 hellothis z Q9ffa4 arabidopsis Q7rf81 plaemodium	. \$1	o aa.	ed) sequence update) annotation update) tein 7, isoform c).	ea; Rhabditida; Rhabditoidea; B.	e E.; to the EMBL/GenBank/DDBJ databases.	elegans: a platform for s Sequencing Consortium.";	cosmid C01B10."; EMBL/GenBank/DDBJ databases.	the EMBL/GenBank/DDBJ databases.	the EMBL/GenBank/DDBJ databases.	the EMBL/GenBank/DDBJ databases.	EMBL/GenBank/DDBJ databases.
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		PRELIMINARY	(TrEMBLrel (TrEMBLrel (TrEMBLrel (Histone ORFNames=C	is elegans. etazoa; Nematoda; Peloderinae; Cae 239;	hulz 99)	7. F.	[3] SEQUENCE FROM N.A. STRAIN=Bristol N2; Blanchard M., Bradshaw "The sequence of C. el. Submitted (MAY-1996) to	33		; ; 03)	NEBristol N2; ase Consortium; ltted (AUG-2004) to the E AF216291; AAF2175.1;
110077777777		RELI	TEB TEB TEN	Bel cazo Pelo 39;	N.A Sc.	N.A 1 N2 613; ortin nce bio 012-	N.A L N2 Bre of of	N.A 1 N2 B-20	ROM N.A. stol N2; (JUL-2003)	N.A. 1 N2;	N. P.
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80		•-	-200 -200 -200 H1	nabd ota; ida	E K B	CB F S = 99 S = 60 S = 60	TB F Bri ague		Bri R.,	Bri- Bri- G A ;	CB F Bri Be C
אוא אוא אא		3W3	MAY OCT 0CT e=h	ary bdit	SEQUENCE FROM N Jedrusik M.A., (Submitted (DEC-	SEQUENCE FROM STRAIN=Bristo. MEDLINE=990699 WormBase Constigence Sequesinvestigating Science 282:20	[3] SEQUENCE FROM STRAIN=Bristol Blanchard M., I "The sequence of State of	[4] SEQUENCE FROM 1 STRAIN=Bristol Waterston R.; Submitted (FBB	[5] SEQUENCE FROM STRAIN=Bristol Wilson R.; Submitted (JUL	SEQUENCE FROM 1 STRAIN=Bristol Wilson R.; Submitted (DEC	
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		RESULT Q9U3W3 ID Q9		8888	8	R R R R R R R R R R R R R R R R R R R	R R R R R R	R R C C R R	R R R R R R	RRRRR	8 2 2 2 2 3 3 8 5 8 5 8 5 8 5 8 5 8 5 8 5 8 5 8 5

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01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 10-OCT-2002 (TrEMBLrel. 22, Hastone H1.
                                                                   26; Conservative
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                                      Best Local Similarity
Matches 26; Conserv
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                           Query Match
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                                                                                                                                                                                                                                             13; Gaps
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Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
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                                                                                                                                                                                               26.4%; Score 82.5; DB 2; Length 60; ilarity 39.7%; Pred. No. 9.5; Conservative 4; Mismatches 21; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Bristol N2;
WormBase Consortium;
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, 'US9757; ARK66020.1; -..
WormBase; WBGene000001858; hil-7.
WormPep; C01B10.5b, CE26856.
SEQUENCE 66 AA; 7005 MW; FDB6D60FB8072D63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Bristol N2;
Blanchard M., Bradshaw H.;
"The sequence of C. elegans cosmid CO1B10.";
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
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Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
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Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases
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Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                         6212 MW; D01ABB4CEC35566D CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Histone hl like protein 7, isoform b.
Name-hil-7; ORFNames=C01B10.5;
                                                                                                                                                                                                                                                                                                              7 AKKVAKTKKVAAKPKVKKASPKKRABPKAKKPVK---
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                  GO, GO:000786; C:nucleosome; IEA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0006334; P:nucleosome assembly; IEA.
InterPro; IPR005919; Histone_H5.
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MEDLINE-99069613; PubMed-9851916;
WormPep; C01B10.5c; CE26857.
                                                                                                                                PRINTS; PR00624; HISTONEHS
SEQUENCE 60 AA; 6212 MW
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Les 25; Conserv
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                                                                                                                                          6 KKEKAYAKAKKAEAKAAKKAKAEAKKYAKAAKAEKKEYAAAEAK---YKAEAAKAAAKEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae, Trypanosoma.
NCBI_TaxID=31285;
                                                       Gaps
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Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
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Thesis (2000), Department of Parasitology, Institute of Zoology,
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25.4%; Score 79.5; DB 2; Length 6:
Best Local Similarity 49.2%; Pred. No. 16;
Matches 29; Conservative 1; Mismatches 24; Indels
26.2%; Score 82; DB 2; Length 66; 42.6%; Pred. No. 11; 1.1ve 7; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=STIB 755;
Grueter E., Betschart B.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ287597; CAB76179.1; -.
SEQUENCE 61 AA; 6059 MW; F600CE6D66D6A73F CRC64;
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Last annotation update)
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Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequ
01-OCT-2003 (TrEMBLrel. 25, Last anno
Histone hl like protein 7, isoform a.
Name-hil-7; ORFNames=C01B10.5;
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MEDLINE=99069613; PubMed=9851916;
WormBase Consortium;
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2 AKASAAPKKAVAK-KAAPKKAAPK-KAVAKKGAPKKAVAKKAAPKKVAPKKVAGKKAAAK 59
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PubMed=14704707, DOI=10.1038/nbt923;
PubMed=14704707, DOI=10.1038/nbt923;
PubMed=14704707, DOI=10.1038/nbt923;
PubMed=14704707, DOI=10.1038/nbt923;
PubMed=14704707, DOI=10.1038/nbt923;
PubMed=1704707, DOI=10.1038/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/nbt923/
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NCBI_TaxID=5702;
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Thesis (2000), Department of Parasitology, Institute of Zoology,
SWITZERLAND.
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizoblaceae; Rhodopseudomonas.
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Submitted (FRB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ207608; CRB76193.1; -20644C3471064DC6 CRC64;
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Last annotation update)
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Last annotation update)
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3; Mismatches
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                                                                                                                                                                                                                                                                                                                      Name=H1A66;
Trypanosoma brucei brucei.
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nes 33; Conservative
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60 KA 61
                                                           61 EA 62
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01-OCT-2000 (
01-OCT-2002 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=427;
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Q6N578;
                                                                                                                                                                                                                    Q9NPJ3;
                                                                                                                                                                                                 Q9NFJ3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AKKYAKKEKAYAKAKKAEAKAAKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKAAAK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBL_TaxID=5702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Grueter E.;
Thesis (2000), Department of Parasitology, Institute of Zoology,
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Pred. No. 22;
2; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 62;
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Grueter E., Betschart B.;
Submitred (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ207603; CAB76188.1; --
SEQUENCE 61 AA; 6012 MW; 7B66DA10A7D33B93 CRC64;
Blanchard M., Bradshaw H.;
"The sequence of C. elegans cosmid C01B10.";
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                      Wilson R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; US8757; AAC47916.1; -.
PIR; T30977; T30977.
                                                                                                                     Waterston R.; Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                          Wilson R.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOTTMBRS: WBGENE00001858; hil-7.
WOTTMPEP; C01B10.5a; CE06736.
SEQUENCE 62 AA; 6453 MW; FF301204D637D406 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7B66DA10A7D33B93 CRC64;
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Last sequence update)
Last annotation update)
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49.2%; Pred. No. 18;
tive 4; Mismatches 21
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Best Local Similarity 46.8*
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STRAIN=Bristol N2;
WormBase Consortium;
                                                                              SEQUENCE FROM N.A. STRAIN=Bristol N2;
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                                                                                                                                                                                                 STRAIN=Bristol N2;
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Gaps

4 ;

15; Indels

73C566FE663AFB08 CRC64;

Score 72; DB 2; Pred. No. 46;

2; Mismatches

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Low W., Lin Q., Stathakis C., Miao M., Fletcher G.L., He Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF306348; AAG22048.1; -
                                . Biol. Chem. 276:11582-11589(2001)
                                                                                                                                                                                                                                                                                                                  23.0%;
52.3%;
                                                                                                                                                                                                                                                        42 AA; 3796 MW;
                                                                                                                                                                                                                                                                                                                                                                                 23; Conservative
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   octodecemspinosus.";
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Best Local Similarity
Matches 22; Conserv
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                                                                                              SEQUENCE FROM N.A.
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05-JUL-2004
05-JUL-2004
05-JUL-2004
                                                                                                                            TISSUE=Skin;
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01-JUN-2003
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Q6MGW9
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PubMed=14671304; DOI=10.1126/science.1088727;
Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,
Heidelberg J.F., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J.,
Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,
Davidsen T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.
Weidman J.F., Khouri H.M., Fasher C.M.;
"Genome of Geobacter sulfurreducens: metal reduction in subsurface
                                                                                                                               Gaps
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MEDLINE=21192197; PubMed=11136728; DOI=10.1074/jbc.M009293200;

Low W.-K., Lin Q., Stathakis C., Miao M., Fletcher G.L., Hew C.L.;

"Isolation and characterization of skin-type, type I antifreeze polypeptides from the longhorn sculpin, Myoxocephalus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Būkaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, statinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei, Acanthomorpha, Acanthopterygii, Percomorpha, Scorpaeniformes, Cottoidei, Cottidae, Myoxocephalus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
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Pred. No. 33;
0; Mismatches 12; Indels
                                                                 Length 66;
                                                                                                                        12; Indels
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Complete proteome; Hypothetical protein.
SEQUENCE 35 AA; 3966 MW; OEGE2B600A034777 CRC64;
66 AA; 6976 MW; EA6E55669063B259 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Longhorn sculpin skin-type antifreeze protein.
Myoxocephalus octodecimspinosis (Longhorn sculpin).
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Last annotation update)
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                                                       Score 76; DB 2;
Pred. No. 33;
2; Mismatches 12
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EMBL; AE017180; AAR36633.1; -.
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l Similarity 50.0%;
24; Conservative
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les 21; Conservative
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Geobacter sulfurreducens.
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NCBI_TaxID=35554;
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                                                              Query Match
Best Local Similarity
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STRAIN-PCA / ATCC
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Sakaki Y., Hattori M., Omura S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis.";
Nat. Biotechnol. 21:226-531(2003).
EMBL; AP005025; BAC68667.1; -
Complete proteome; Hypothetical protein.
SEQUENCE 57 AA; 5950 MW; 4C019AD92139FA43 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>ي</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C., Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T., Kikuchi H., Shiba T., Sakaki Y., Hattori M.; "Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=MA-4680;
MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
                                                                                                                                                                                                                                                                                                                                                                                                  Streptomyces avermitilis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21; Indels
17 AEAKAAKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKAAAK 60
                                                        3 APAKAAAKTAAD----AKAAAAKTAADALAAANKTAAAAKAAAK 42
                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 22.5%; Score 70.5; D
1 Similarity 41.5%; Pred. No. 78;
22; Conservative 5; Mismatches
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Pred. No. 78;
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                                                                                                                                                                                                                                                          Created)
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                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                     (TrEMBLrel. 24, (TrEMBLrel. 24,
                                                                                                                                                                                                                                                    (TrEMBLrel. 24, (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                       OrderedLocusNames=SAV957;
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Score 67; DB 2; Length 44;
Pred. No. 1.2e+02;
                                                                                     Histone-like protein (Fragment).
Lactobacillus delbrueckii (subsp. lactis).
Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
                                                                                                                                                                               Langenheim J.F., Ulrich R.L.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AR496145; AAQ06805.1; -.
NON TER 44 44
                                                                                                                                                                                                                                                         44 AA; 4634 MW; CAC365D7CFC6A162 CRC64;
                                                             05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                    1 AKKYAKK--EKAYAK-AKKAEAKAAKK-AKAEAKKYAK 34
                                                                                                                                                                                                                                                                                                                                                              7 AKKSAKKSTKKAAKKSAKKSTKKAAKKSAKKSTKKAAK
                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                             64
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                    Created)
                          PRT;
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                                                                                                                                                                                                                                                                                  21.4%;
60.5%;
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                                                                                                                                                                                                                                                                                                             23; Conservative
                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Coxiellaceae; Coxiella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein
                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coxiella burnetii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                         Lactobacillus.
NCBI_TaxID=29397;
                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                            STRAIN=ATCC 4797;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CBU1932; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 AKA 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Q83AG7;
01-JUN-2003
01-JUN-2003
                                      Q711Y2;
05-JUL-2004
                                                                                                                                                                                                                                                       SEQUENCE
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RESULT 13
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                                                                       SEQUENCE FROM N.A.
STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
PubMed=14752164; DOI=10.1126/science.1093027;
Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,
Keller H., Lambert C., Evans K.J., Goesmann A., Meyer F.,
Sockett R.E., Schuster S.C.;
"A predator unmasked: life cycle of Bdellovibrio bacteriovorus from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            core; Spermatogenesis.
S -> T (possible variant of component I).
A -> T (in component II).
S -> T (possible variant of component I).
S -> T (possible variant of component I).
                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from Mytilus californianus.";
Bur. J. Biochem. 182:569-576(1989).
-!- FUNCTION: Involved in nuclear basic protein transition: histones
are replaced by spermatid specific proteins which are themselves
replaced by protemines in late spermatids.
-!- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence and characterization of the sperm-specific protein phi 3
                 Bacteria, Proteobacteria, Deltaproteobacteria, Bdellovibrionales,
Bdellovibrionaceae, Bdellovibrio.
NCBI_TaxID=959;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sperm-specific protein Phi-3 (PL-IV).
Mytilus californianus (California mussel).
Bukaryota, Metazoa, Mollusca, Bivalvia, Pteriomorphia, Mytiloida,
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                                                                                                                                                                                                                                             21.9%; Score 68.5; DB 2; Length 43; 54.5%; Pred. No. 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 45;
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78A68DF2CB77C4E1 CRC64;
                                                                                                                                                                                                                   43 AA; 4598 MW; 11AB9E005A80493C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 12, Created)
(Rel. 12, Last sequence update)
(Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                        45 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=89325302; PubMed=2666130;
                                                                                                                                                                genomic perspective.";
Science 303:689-692(2004).
EMBL; BX842656; CAE81160.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mytiloidea; Mytilidae; Mytilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nuclear protein; Nucleosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4912 MW;
            3dellovibrio bacteriovorus.
OrderedLocusNames=Bd3800;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR, S04941; S04941.
PIR; S10544; S10544.
PIR; S10545; S10545.
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les 24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VCBI_TaxID=6549;
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                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-Nine Mile phase I / RSA 493; MEDLINE-22608657; PubMed=12704232; DOI=10.1073/pnas.0931379100; Seshadri R., Paulgen I.T., Eisen J.A., Read T.D., Nelson K.E., Nelson W.C., Ward N.L., Tettellin H., Davidsen T.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Brinkac L.M., Madupu R., Dodson R.J., Khouri H.M., Lee K.H., Carty H.A., Scanlan D., Heinzen R.A., Thompson H.A., Samuel J.E., Fraser C.M., Heidelberg J.F.; "Complete genome sequence of the Q-fever pathogen, Coxiella burnetii.";
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ب
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
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SEQUENCE 64 AA; 7249 MW; BOABICDC6B0F4C30 CRC64;
                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             broc. Natl. Acad. Sci. U.S.A. 100:5455-5460(2003)
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PRELIMINARY;

Q9C2J3 RESULT 15 Q9C2J3

ACCOCCOS ON THE BEAR ON THE BE

### 1; This Page Blank (usptc) SEQUENCE FROM N.A. Schulsel J., Brandt P., Fartmann B., Holland R., Schulte U., Aign V., Hoheisel J., Brandt C.; Newes H.W., Mannhaupt G.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. 1; Gaps 6 KKEKAYAKAKKAEAKAAKKAKAEAKKYAKAAKA-EKKEYAAAEAKYKAEAAK 56 Neurospora crassa. Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Sordariales; Sordariaceae; Neurospora. NCBI_TaxID=5141; Query Match 20.0%; Score 62.5; DB 2; Length 62; Best Local Similarity 36.5%; Pred. No. 3.6e+02; Matches 19; Conservative 10; Mismatches 22; Indels GEGURNCE FROM N.A. German Neurospora genome project; German Neurospora genome project; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AL513408; CAC28556.1; InterPro; IPR007513; Four_F5. Pfam; PF04419; 4F5; 1. Hypothetical protein. SEQUENCE 62 AA; 6798 MW; C145D10EF2855C73 CRC64; Q9C2J3; 01-UJN-2001 (TrEMBLrel. 17, Created) 01-JJN-2001 (TrEMBLrel. 17, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Hypothetical protein 61D6.060; Name=61D6.060; 62 AA. Search completed: June 3, 2005, 10:55:51 Job time: 174 secs PRT;

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OM protein - protein search, using sw model

Run on:

3, 2005, 10:37:59; Search time 158 Seconds (without alignments) 161.558 Million cell updates/sec

US-10-792-311-4 313 Perfect score:

1 AKKYAKKEKAYAKAKKAEAK......EAKYKAEAAKAAAKEAAYEA 66 Seguence:

**BLOSUM62** Scoring table:

Gapop 10.0 , Gapext 0.5

1029624 Total number of hits satisfying chosen parameters: 2105692 segs, 386760381 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 66

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

•• Database

A Geneseq 16Dec04:* 1: geneseqp1980s:* 2: geneseqp1990s:*

geneseqp2003as:* geneseqp2000s:* geneseqp2001s:* geneseqp2002s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

#### SUMMARIES

	lon	Copolymer	Copolymer	Copolymer	Copolymer	Peptide u	Nucleic a	Tumour ne	Peptide u	High affi	Sea urchi	Yeast zuo	Nucleic a	Peptide u	Nucleic a	Nucleic a	Human lin	Human lin	Chicken h	Yeast zuo	Polycatio	Protamine	Polycatio	Protamine	Histone H	Human his
	Description	Aay82574	Aay82573	Aay82572	Aay82571	Ado43176	Aaw24449	Abg71043	Ado43172	Aar28871	Ado04487	Ads15345	Aaw08392	Aaw38225	Aaw69201	Aaw52872	Aae13239	Aae13240	Ado04488	Ads15346	Aar90180	Aaw06686	Aar90181	Aaw06688	Aay34069	Aay57367
	QI	AAY82574	AAY82573	AAY82572	AAY82571	AD043176	AAW24449	ABG71043	ADO43172	AAR28871	AD004487	ADS15345	AAW08392	AAW38225	AAW69201	AAW52872	AAE13239	AAE13240	ADO04488	ADS15346	AAR90180	AAW06686	AAR90181	AAW06688	AAY34069	AAY57367
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*	Query	100.0	63.3	38.5	33.7	33.1	32.6	31.3	31.2	30.0	28.6	28.6	26.8	26.8	26.8	26.8	26.8	26.7	26.7	26.7	26.2	26.2	26.2	26.2	26.0	26.0
	Score	313	198	120.5	105.5	103.5	102	98	97.5	94	89.5	89.5	84	84	84	84	84	83.5	83.5	83.5	82	82	82	82	81.5	81.5
	Result No.	п	7	m	4	S	9	7	80	6	10	11	12	13	14	. 15	16	17	18	19	20	21	22	23	24	25

Ado43179 Peptide u Abu21642 Protein e Aaw08401 Nucleic a Aaw69205 Nucleic a Aag40992 Zea maye Adb08170 Peptide m Ade10601 Structura Adx15620 Nucleatin Aag40982 Zea mays Aaw24450 Nucleatin Aay98493 Peptide # Aay59038 Peptide u Aay59038 Peptide u	
ADO41179 ABU21642 AAW08401 AAW68205 AAG40992 AAB08170 ADK15620 ADK15620 AAX498493 AAX598493 AAX59038	AAD42840 AAU18248 ABG92669 AAC25386 AAY59040 AAY59040
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# ALIGNMENTS

Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyalinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; permisis; pemphigus vulgaris; systemic lupus erythematosus. Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:4. AAY82574 standard; peptide; 66 AA. (first entry) 28-JUL-2000 RESULT 1 AAY8257 

Unidentified

WO200018794-A1.

06-APR-2000.

99WO-US022402. 24-SEP-1999; 98US-0101693P. 25-SEP-1998; (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.

Lis D; 3ad A, WPI; 2000-317499/27.

Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.

Claim 10; Page 14; 72pp; English.

AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides

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treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases but diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune thrombocytopaenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myacedema, myasthemia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated mediated diseases which can be treated include host-versus-make for graft-versus-host disease, and delayed-type hypersensitivity. The goopsties of the invention have defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which markes them ideal for use as molecular weight markers
                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glatitamer acetate; autoimmune disease; antiarthriti; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; cronn's disease; ohronic immune thrombocytopaemia purpura; colitis; diabetes mellitus; Graves disease; Oliliain.Barre's syndrome; psorlassis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AKKYAKKEKAYAKAKKAEAKAAKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKAAAK
                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:3.
  are used as molecular weight markers for glatiramer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Copolymer; molecular weight marker; TV-marker; immune disease;
                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 313; DB 3; Length 66; 100.0%; Pred. No. 7.3e-24; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pemphigus vulgaris; systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY82573 standard; peptide; 56 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.
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                                                                                                                                                                                                                                                                                                                                                                            28-JUL-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 EAAYEA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EAAYEA 66
                                                                                                                                                                                                                                                                                                                                                             Sequence 66 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200018794-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lis D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-APR-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY82573;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 2
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Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyrodi; antiinflammatory; antidabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; (Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                    1 AKKYAKKEKAY---AKKAE-KAAK---KAEAKAY-KAAEAKKK----AEAKYKAEAAKAAAK 50
                                                                                                                                                                                                                                                                                                                                                         1 AKKYAKKEKAYAKAKKAEAKAAKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKAAAK 60
                              to AAY82577 represent specifically claimed copolymer molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                    10; Gaps
                                                                                                                                                                                                                                                                                                             63.3%; Score 198; DB 3; Length 56; 80.3%; Pred. No. 1.4e-12; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY82572 standard; peptide; 45 AA.
          Claim 10; Page 14; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US022402.
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                                                                                                                                                                                                                                                                                                                                   53; Conservative
                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                     61 EAAYEA 66
                                                                                                                                                                                                                                                                                                                                                                                                                           EAAYEA 56
                                                                                                                                                                                                                                                                                         Sequence 56 AA;
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                                                                                                                                                                                                                                                                                                               Query Match
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(YEDA ) YEDA RES & DEV CO LTD

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of the invention are used as molecular weight markers for glatization catetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include arthritic conditions, demyelinating diseases. Such diseases include arthritic conditions, demyelinating diseases. Such diseases include arthritic conditions, demyelinating cliseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, autoimmune basmolylic anaemia, autoimmune cophoritis, autoimmune thyroiditis, autoimmune uveoretinitis, contact disease, chronic immune thrombocytopaenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, diabetes disease, diabetes defined molecular weights and physical prophypeptides of the invention have defined molecular weight markers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and amino acid composition corresponding to the copolymer. The polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyromimetic; hemostetic; antipsoriatic; dermatological; antidiabetic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; crohn's disease; chronic immune thrombooytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis;
                                                                                                                                                                                                                                                                       Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.
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pemphigus vulgaris; systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38.5%; Score 120.5; DB 3; Length 45; 71.1%; Pred. No. 5.1e-05; Live 0; Mismatches 6; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAAYEA 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY82571 standard; peptide; 35 AA
                                                                                                                                                                                                                                                                                                                                                                                                               Claim 10; Page 14; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US022402
(TEVA-) TEVA PHARM USA INC
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Best Local Similarity
                                                                                                                                                                                  WPI; 2000-317499/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 45 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200018794-A1.
                                                                                              Gad A, Lis D;
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MAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer acctate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune thyroiditis, autoimmune uveoretinitis, Crohn's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disease, chronic immune thrombocytopaenia purpura, collitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxodema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated mediated disease which can be treated include host-versus-graft disease, polypeptides of the invention have defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as molecular weight markers
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------KAKAAEAAK 29
                                                                                                                                                                                        Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.7%; Score 105.5; DB 3; Length 35; 43.9%; Pred. No. 0.0012; Live 2; Mismatches 4; Indels 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nano-barcode; scanning probe microscopy; probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide used for coded probe synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADO43176 standard; peptide; 56 AA.
                                                                                                                                                                                                                                                Claim 10; Page 14; 72pp; English.
                  25-SEP-1998; 98US-0101693P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-SEP-2003; 2003WO-US029726.
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                                                                                                                                                  WPI; 2000-317499/27.
                                                    (YEDA ) YEDA RES & (TEVA-) TEVA PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 EAAYEA 66
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                                                                                                                Lis D;
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Gaps

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                                                                                                                                                    Detecting, identifying and sequencing of biomolecules using controlled alignment of nano-barcodes encoding specific information for scanning probe microscopy, useful in the fields of molecular biology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene therapy; binding complex; lysis agent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid transporter useful in gene therapy - contains binding complex associated with surface and nuclear ligands and lysis agent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JTS-1; K8; alpha helix; endosome; lysosome; nucleus targeting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 8; Length 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 103.5; DB 8; Length
Pred. No. 0.0031;
0; Mismatches 20; Indels
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                                                                                                                                                                                                                            Example 2; Page 44; 63pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW24449 standard; peptide; 46 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95US-00484777.
20-SEP-2002; 2002US-00251152.
19-SEP-2003; 2003US-00667004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.1%;
56.9%;
                                                                                    Su X, Yamakawa M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid transporter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-052345/05.
                                                                                                                      WPI; 2004-399960/37
                                                (ITLC ) INTEL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Màtch
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 56 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9640958-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Smith LC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW24449;
                                                                                    Chan S,
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AAW24434-W24459 are nucleic acid (NA) binding peptides, capable of both condensing and stabilising a NA. The peptides can be conjugated to a lytic peptide to form a nucleic acid transporter system. The lysis agent forms an alpha-helical structure. The transporter system is used to deliver nucleic acid to a cell and for treating humans by gene therapy. By taking advantage of the characteristics of both the lysis agents and the binding molecules, delivery of the nucleic acid is enhanced. Specific lysis agents are capable of releasing the nucleic acid into the cellular interior from the endosome. Release is efficient without endosomallysosomal degradation. Once released the binding complexes help target the nucleic acid to the nucleus
                                                                                                                                                                                                                                                5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumour neoangiogenesis; peptidase substrate; tumour related disorder; tumour-selective intravascular coagulation inducing molecule; blood clotting; tumour vascularisation; tumour growth control;
                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumour neoangiogenesis associated peptidase substrate peptide #7.
                                                                                                                                                                                                                                                5
                                                                                                                                                                                                                  / Match 32.6%; Score 102; DB 2; Length 46; Local Similarity 64.4%; Pred. No. 0.0035; les 29; Conservative 5; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                              9 KAYAKAK-KAEAKAAKAKAEAKKYAKA-AKAEKKEYAAAEAKYK 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference 25. .30 /note= "Optionally absent"
Misc-difference 31. .36 /note= "Optionally absent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Optionally absent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19. .24
/note= "Optionally absent"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ote= "Optionally absent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .54
.te= "Optionally absent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13. .18
/note= "Optionally absent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Optionally absent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYLO-) UNIV CATHOLIQUE LOUVAIN.
                                                                                                                                                                                                                                                                                                                                                                                  ABG71043 standard; peptide; 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JAN-2001; 2001EP-00870017.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JAN-2002; 2002WO-EP000951.
                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             heparin-binding peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7. .12
/note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference 43
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Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                         Sequence 46 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          16-DEC-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                     Query Match
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                                                                                                               The invention describes tumour-selective intravascular coagulation inducing molecules. The molecules are useful as a medicine and in the manufacture of a medicament for the treatment and/or prevention of tumour related disorders. The compounds are able to induce blood clotting at tumour sites resulting in the disruption of the tumour vascularisation and consequently in the control of tumour growth. This sequence represents a hepain-binding peptide, a postively charged polymer that can be incorporated into a substrate for extracellular hydrolases releasable by tumour or neoangiogenic endothelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is that of a peptide of potential use for production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of a coded probe useful in the method of the invention. The invention provides methods, apparatus and compositions for the detection, identification and/or sequencing of biomolecules, such as nucleic acids or proteins. Coded probes comprising a probe molecule attached to one or more nano-barcodes are allowed to bind to target molecule(s). After binding and separation from unbound coded probes, the bound coded probes are aligned on a surface and analysed by scanning probe microscopy (SPM). An approach to coded probe synthesis entails creating polymer scaffolds to which nano-tag elements are attached through post-polymer assembly.
                                 tumor-selective intravascular coagulation inducing molecules useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detecting, identifying and sequencing of biomolecules using controlled alignment of nano-barcodes encoding specific information for scanning probe microscopy, useful in the fields of molecular biology.
                                                                                                                                                                                                                                                                                                                                                                                             5 AKKEKAYAKAKKA-BAKAAKKAKABAK-KYAKAAKABKKEYAA--ABAKYKABAAKAA 58
                                                                                                                                                                                                                                                                                                                                                                                                               4; Gaps
                                                                                                                                                                                                                                                                                                                        31.3%; Score 98; DB 5; Length 60; 53.4%; Pred. No. 0.012;
                                                                                                                                                                                                                                                                                                                                                          16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nano-barcode; scanning probe microscopy; probe.
                                                                                                                                                                                                                                                                                                                                                          7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide used for coded probe synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Page 43; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADO43172 standard; peptide; 49 AA
                                                                                 Claim 20; Page 27; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-SEP-2003; 2003WO-US029726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-SEP-2002; 2002US-00251152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-SEP-2003; 2003US-00667004
                                                   control of tumor growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Su X, Yamakawa M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                           31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-399960/37.
WPI; 2002-706887/76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ITLC ) INTEL CORP.
                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2004038037-AZ.
                                                                                                                                                                                                                                                                                          Sequence 60 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADO43172;
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                                                                                                                                                                                                                                                                                                                                          Best Loca
Matches
                                   dev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AD04317
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For example, nano-tag elements can be attached to a peptide that has active groups (in the present case, lysine) at specific appropriately spaced sites. The peptide is then exposed to a mono-functionalised nanotag element and all of the active sites are modified. The methods allow high speed of obtaining sequence data, low cost of sequencing run, high speed of obtaining sequence data, low cost of sequencing and high efficiency in terms of operator time, and sensitive and accurate detection and/or identification of nucleic acids with low incidence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   glycopeptide; mannose; mannosylated; glycosylated; mannose receptor; macrophages; monocytes; destroy; cytotoxicity; label; image; alter; macrophage processing of antigen; MFC restriction; inflammation; inflammatory diseases; macrophage secretory products; Crohn's disease; legionnaires disease; mononuclear phagocytes; HIV; AIDS; lysosomal storage diseases; Gaucher's disease, asthma; alveolar macrophages metastasis; systemic macrophages; deliver; antigenic peptides; prevent transplant rejection; organ transplantation; antitumour agents; cancer; toxins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "opt may have mannose, fucose, glucose or N-Ac-glucosamine." 28\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "opt may have mannose, fucose, glucose or N-Ac-
glucosamine."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "opt may have mannose, fucose, glucose or N-Ac-
mine."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                glucose or N-Ac-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "opt may have mannose, fucose, glucose or N-Ac-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "opt may have mannose, fucose, glucose or N-Ac-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or N-Ac-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fucose, glucose or N-Ac-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or N-Ac-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "opt may have mannose, fucose, glucose or N-Ac-glucosamine. May also have non interfering substits."
                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                             62
                                                                                                                                                                                                                                                                                                       48
                                                                                                                                                                                                                                                                             10 AYAKAKKAEAKAAKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKAAAKEA
                                                                                                                                                                                                                                                                                                       aaaaaakaaaaakaaaaakaaaaaka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fucose, glucose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glucose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High affinity macrophage mannose receptor ligand compound #9.
                                                                                                                                                                                                         31.2%; Score 97.5; DB 8; Length 49; 58.5%; Pred. No. 0.011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fucose,
                                                                                                                                                                                                                                         17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             may have mannose,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         may have mannose,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "opt may have mannose,
                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                  AAR28871 standard; peptide; 46 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glucosamine."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glucosamine."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glucosamine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                             31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note=
                                                                                                                                             false positive results.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (revised)
                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                           Sequence 49 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR28871;
                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                RESULT 9
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Modified-site

Macroscopic membrane; cell growth; EAK16; Z-DNA binding protein; zuotin; medical product; suture; artificial skin; internal lining; slow-diffusion drug delivery system; protein-type drug; erythropoietin; haemoglobin; insulin; cell adhesion; cell migration; Alzheimer's disease; scrapie infection; sea urchin; histone; HI; variant.

Sea urchin histone H1 variant protein.

29-JUL-2004

ADO04487 standard; protein; 60 AA.

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This compound represents a glycopeptide effective in inhibiting the binding of labelled mannosylated BSA to mannose receptors. Mannose receptors are uniquely found on macrophages and not on monocytes. Glycopeptides are uniquely found on macrophages and not on monocytes specifically, to image, label, destroy or otherwise alter their antigen processing function. In addition they can be conjugated to solid supports and used to purify mannose receptors from a variety of sources. They are useful in the treatment of inflammatory diseases driven by macrophage secretory products eg. Crohn's disease; infectious diseases in which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New high affinity mannose receptor ligand cpds. - for treating diseases mediated by macrophage activity e.g. asthma, inflammatory diseases and
                                                                                                                         /note= "opt may have mannose, fucose, glucose or N-Ac-glucosamine."
                                                                                                                                                                                                                /note= "opt may have mannose, fucose, glucose or N-Ac-glucosamine."
/note= "opt may have mannose, fucose, glucose or N-Ac-
                                     'note= "opt may have mannose, fucose, glucose or N-Ac-
lucosamine."
                                                                                                                                                                            note= "opt may have mannose, fucose, glucose or N-Ac-
                                                                                                                                                                                                                                                                     /note= "opt may have mannose, fucose, glucose or N-Ac-
                                                                                        or N-AC
                                                                                                                                                                                                                                                                                      glucosamine. May also have non interfering substits."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        macrophages harbour replicating infectious agents eg. Legionnaires
                                                                            /note= "opt may have mannose, fucose, glucose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Page 21; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                             92WO-US003609.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           infectious diseases, e.g. HIV
             glucosamine."
                                                                                                                                                                                                                                                                                                                                                                                                         91US-00694983
                                                                                                                                                                                                glucosamine.
                                                                                                                                                                                                                                                                                                                                                                                                                                     (UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1992-398516/48.
                             Modified-site
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                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                  WO9219248-A1
                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                                                         3-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stahl PD;
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Novel EAK16 protein incorporated into macroscopic membranes, useful in biomaterial applications such as medical products, artificial skin or internal linings, slow-diffusion drug delivery systems for in vitro cell

Example 5; SEQ ID NO 16; 56pp; English.

growth.

Lockshin C;

Dipersio CM,

Rich A,

Holmes T, Zhang S, PI; 2004-356208/33

DIPERSIO C M. LOCKSHIN C.

HOLMES T. ZHANG S.

RICH A.

(HOLM/) (ZHAN/) (RICH/) (DIPE/) LOCK/)

92US-00973326. 94US-00293284. 97US-00824515.

28-DEC-1992; 22-AUG-1994;

26-MAR-1997;

.7-MAR-2003; 2003US-00390472

Arbacia punctulata

US2004087013-A1.

06-MAY-2004.

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disease; viral infections involving monouclear phagocytes eg. HIV and lysosomal storage diseases, in which macrophages are principally involved eg. Gaucher's disease; asthma mediated by alveolar macrophages; and in controlling metastasis, mediated by systemic macrophages. The peptides can also be used to deliver antigenic peptides as conjugates to a macrophage to marshal an immune response; also self peptides to prevent issue transplant rejection. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30.0%; Score 94; DB 2; 64.6%; Pred. No. 0.022; iive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 46 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loca
Matches
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The invention relates to a method for in vitro cell culture which involves adding a macroscopic membrane that is formed by self-assembly of amphiphilic peptide in an aqueous solution containing monovalent metal cations to a cell culture medium comprising cells, thus forming a membrane/culture mixture, maintaining the mixture under conditions sufficient for cell growth. The invention also relates to EAK16 peptide cellsicient for cell growth. The invention also relates to EAK16 peptide into the macroscopic membranes are useful in biomaterial applications such as medical products (e.g., sutures), artificial skin or internal into growth or culture and support for artificial tissue for in vitro cell crowth or culture and support for artificial tissue for in vivo use, as slow-diffusion drug delivery systems supports for in vivo use, as slow-diffusion drug delivery whicle for delivering protain-type drugs e.g., erythropoietin, synthetic haemoglobin, insulin, etc., useful as conductive biopolymer for culturing cell monolayers, for promoting cell adhesion and migration, useful as experimental models for Alzheimer's disease and scrapic infection. The present sequence is sea urchin histone invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28.6%; Score 89.5; DB 8; Length 6 56.8%; Pred. No. 0.081; ive 2; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 KKYAKKEKAYAKAKA---EAKAAKKAKAEAKKYAKAAKAEKKE 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 56.8
les 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 60 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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3

Gaps

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8; Indels

31; Conservative

ठे

28 45

12 AKAKKAEAKAAKKAK-AEAKKYAKAAKAEKKEYAAAEAKYKAEAAKAA

RESULT 10 ADO04487

nucleic acid; condensing peptide; transfection; mammalian cell;

Nucleic acid condensing peptide (NBC1)

(first entry

19-SEP-1997

AAW08392;

Synthetic virus like particle, heteropeptide, polydispersion; gene therapy; self assembly.

AAW08392 standard; peptide; 61 AA.

/note= "S-acetoamidomethylated"

Location/Qualifiers

Modified-site

Synthetic

WO9641606-A2

27-DEC-1996

```
The invention describes a method of culturing (M1) cells, in vitro. The cell culture involves adding a macroscopic membrane which is formed by self-assembly of amphiphilic peptides in an aqueous solution containing monovalent metal cations, where the peptides have alternating hydrophobic and hydrophilic amino acids and are complementary and structurally compatible, to a cell culture medium comprising cells, thus forming a membrane/culture mixture, and maintaining the mixture under conditions sufficient for cell growth. (M1) is useful for culturing a macroscopic membrane utilised in biomaterial applications e.g., slow-diffusion drug delivery systems, artificial skin or separation matrices, or as experimental models for Alzheimer's disease and scrapic infection e.g., liver cirrhosis, kidney amyloidosis, or other protein conformational claseases. (M1) enables in vitro culturing of macroscopic membrane that is stable in aqueous solution, serum and ethanol, highly resistant to heat, alkaline and acidic pH, chemical denaturants and proteolytic digestion, and is non-cytotoxic. This is the amino acid sequence of a region found in sea urchin histone HI delta which is homologous to yeast DNA binding protein zuotin from which amphiphilic peptides capable of forming membrane can be isolated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Culturing cells, in vitro, by adding macroscopic membrane formed by self-assembly of amphiphilic peptides and monovalent metal cations, to form culture mixture, and maintaining culture mixture under conditions for
                                                                                                                                                                                                  cell culture; macroscopic membrane; amphiphilic peptide; biomaterial; slow-diffusion drug delivery system; artificial skin; separation matrix; Alzheimer's disease; scrapie; liver cirrhosis; kidney amyloidosis; protein conformational disease; yeast; DNA binding protein; zuotin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lockshin C;
                                                                                                                                                              Yeast zuotin homologue sea urchin H1 delta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dipersio CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 5; SEQ ID NO 16; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MASI ) MASSACHUSETTS INST TECHNOLOGY.
                                        ADS15345 standard; protein; 60 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-00824513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92US-00973326
94US-00293284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhang S, Rich A,
                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                            Paracentrotus lividus
                                                                                                                                                                                                                                                                                      sea urchin; H1 delta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-707224/69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 60 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-DEC-1992;
22-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                  US6800481-B1
                                                                                                                      16-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Holmes T,
                                                                                ADS15345;
RESULT 11
                       ADS15345
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nucleic acid molecule and a non-covalently associated set of nucleic acid condensing peptides (NACP), e.g. the present peptide, where each NACP is a heteropeptide, and the NACP set has low polydispersion. The SVLP, which is for transfecting a nucleic acid molecule into a mammalian cell, can be used for gene therapy. It is self assembling, and can be designed to target a particular cell or tissue type and deliver the nucleic acid molecule into its chromosomal or extrachromosomal sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 KKYAKKEKAYAKAKAEAKAAKKAKAKAEAKKYAKAAKAEK-KEYAAAEAKYKAEAAKAAA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A novel synthetic virus like particle (SVLP), comprises a recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.8%; Score 84; DB 2; Length 61;
45.8%; Pred. No. 0.29;
tive 8; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide used in vaccine preparation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW38225 standard; peptide; 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l Similarity 45.8
27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 61 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW38225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
AAW38225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
SXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 89.5; DB 8; Length 60;
Pred. No. 0.081;
2; Mismatches 14; Indels
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28.6%;

Conservative

Local Similarity hes 25; Conser

Best Loca Matches

ሯ

RESULT 12 AAW08392

Query Match

7

comprising recombinant

Synthetic virus-like particles for gene therapy - c nucleic acid and nucleic acid condensing peptide(s)

Claim 38; Page 123; 193pp; English.

Welsh JH;

Cunliffe VT,

Wilks PE,

Craig RK,

Thatcher DR,

WPI; 1997-065278/06.

(THER-) THEREXSYS LTD

1996;

.2-FEB-1996

95GB-00019304. 95US-0004285P. 95GB-00025955. 95US-0008952P.

25-SEP-1995; 19-DEC-1995; 19-DEC-1995;

96US-0011531P 96US-00660231

95US-0000124P 95GB-00013399

08-JUN-1995

30-JUN-1995 21-SEP-1995

96WO-GB001396

10-JUN-1996;

Craig R;

```
This sequence represents a nucleic acid condensing peptide that was identified using the method of the invention. The method is for screening contestions for the ability to optimally transfect cells with a nucleic acid molecule (NAM), and comprises: (a) detecting a change in the surface plasmon resonance (SPR) of a nucleic acid immobilised on a sensor chip and exposed to a solution of a test peptide, where the change in SPR occurs upon binding of the peptide to and dissociation of the peptide from the immobilised nucleic acid, to permit calculation of the cequilibrium constant (K(d)) (or apparent dissociation of the cequilibrium the peptide having K(d), with a value of Ix10-12 to Ix10-6 or kd, with a value of Ix10-6 to Ix10-11. The methods can be used for optimising the efficiency of transfecting cells with NAMs. They permit the selection of peptides having binding capacity for nucleic acid to provide a gene delivery complex that is stable in the bloodstream, targetable to selected tissue types, and capable of efficient transport into the cytoplasm and to the nucleus
                                                                                                                                                                                                                                                                                                                          Transfection of cells with nucleic acid(s) - comprises use of peptide(s) screened for interaction with nucleic acids on sensor chip by surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KKRKVEKKSPKKAKKPAAKSPAKAKAVK-PKAAKPKKPKKKRKVEKKSPKKAKKPAA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 KKYAKKEKAYAKAKKAEAKAAKKAKAEAKKYAKAAKAEK-KEYAAAEAKYKAEAAKAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 26.8%; Score 84; DB 2; Length 61; Best Local Similarity 45.8%; Pred. No. 0.29; Matches 27; Conservative 8; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                condensing peptide; episomal DNA expression icted gene expression; gene therapy; cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              episomal DNA
                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 24-25; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "C(Acm)-OH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW52872 standard; peptide; 61 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid condensing peptide.
                                                                                                                                                                                            THERAPEUTICS LTD
                                                                                                                           96US-0033908P.
96GB-00026992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97WO-GB002213.
                                                                                   97WO-GB003523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tissue-restricted gene
                                                                                                                                                                                                                                                                                 WPI; 1998-377790/32
                                                                                                                                                                                                                                                                                                                                                                     plasmon resonance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 61 AA;
                                                                                                                                                                                            (COBR-) COBRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
Modified-site
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WO9828626-A1
                                                                                                                           23-DEC-1996;
27-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-JUL-1998
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                                                                                   23-DEC-1997;
                                                                                                                                                                                                                                       Thatcher DR,
                                        02-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW52872;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW52872
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (APC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid condensing peptide; cell transfection; gene delivery system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence was used in the development of a novel method of vaccinating a mammal against a disease. The method comprises administering a nucleic acid encoding a 1st epitope and a peptide comprising a 2nd epitope, such that the nucleic acid and peptide are taken up by and expressed in a professional antigen presenting cell (APC) of the mammal, where an immune response is elicited in the mammal to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vaccination of mammals against disease - by introducing nucleic acid encoding a first epitope and a peptide comprising a second epitope into antigen presenting cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   epitope. The method can be used for immunisation against infectious against or disease targets, e.g. tumours. The method can be also be used to generate both prophylactic and therapeutic immune responses. The method provides for stimulation of class I and II MHC presentation by providing antigen to an APC in the form of an endogenously synthesised protein, i.e. a nucleic acid encoded epitope, and an exogenously synthesised synthesised protein. The method provides an enhanced and long lasting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 KKYAKKEKAYAKAKKAEAKAAKKAKAEAKKYAKAAKAEK-KEYAAAEAKYKAEAAKAAA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "modified with acetamidomethyl (Acm) protecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Gaps
                 Vaccination; immunisation; infectious agent; disease target; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 84; DB 2; Length 61; Pred. No. 0.29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid condensing peptide NBC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 23; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW69201 standard; peptide; 61 AA
                                                                                                                                                                                                                                                       96GB-0014548.
96GB-0024116P.
                                                                                                                                                                                          97WO-GB000396.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26.8%;
                                                                                                                                                                                                                                     96GB-00002777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 45.8°
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              group"
                                                                                                                                                                                                                                                                                                                                            (THER-) THEREXSYS LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-415072/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 61 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
Modified-site
                                                                                                                                                                                                                                                         30-APR-1996;
11-JUL-1996;
16-AUG-1996;
                                                                                                       W09728818-A1
                                                                                                                                                                                          12-FEB-1997;
                                                                                                                                                                                                                                     12-PEB-1996;
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                                                                                                                                                 14-AUG-1997
                                                            Synthetic.
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7

Gaps

5

5

expression vector;

RESULT 14

ò g 

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This sequence represents a nucleic acid condensing peptide, that can be used to deliver the vector of the invention. The vector is a self-replicating, episomal DNA expression vector (A) for expressing a gene (I) comprises: (a) a self-replicating origin of replication (ori) and (b) a locus control region (LCR), or its component, that when linked to (I) alliects expression of (I) in a tissue-restricted manner. (A) and the vector pair are used for tissue-restricted expression of (I) in cultured cells; in vivo, particularly for gene therapy, e.g. of cancer, or exvivo, for subsequent return of transfected cells. Transgenic animals are used to test fidelity and efficacy of tissue-restricted expression before clinical trials, also for long-term production of (I)-encoded proteins. (A) provide stable gene expression over at least 10-15 cell generations
                                                                                                                                                                                                                 Self-replicating, episomal vector for tissue-restricted expression of genes - includes origin of replication and locus control region, optionally used with second vector expressing replication protein.
                                                                                                                                                                                                                                                                                                              Disclosure; Page 33; 66pp; English.
                  96GB-00017214.
96US-0025040P.
                                                                                   (MEDI-) MEDICAL RES COUNCIL.
                                                                                                                                  Grosveld FG;
                                                                                                                                                                            WPI; 1998-169179/15.
                  16-AUG-1996;
28-AUG-1996;
                                                                                                                                  Antoniou M,
```

Sequence 61 AA;

2 KKYAKKEKAYAKAAKKAEAKAAKKAKAEAKKYAKAAKAEK-KEYAAAEAKYKAEAAKAAA 59 3 KKRKVEKKSPKKAKKPAAKSPAKAKAKAVK-PKAAKPKKKFKVEKKSPKKSPKKAKKPA 60 2; Gaps Query Match 26.8%; Score 84; DB 2; Length 61; Best Local Similarity 45.8%; Pred. No. 0.29; Matches 27; Conservative 8; Mismatches 22; Indels ઠ

5

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Search completed: June 3, 2005, 10:52:53 Job time: 159 secs

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Run on:

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3, 2005, 10:56:01 ; Search time 138 Seconds
(without alignments)
165.325 Million cell updates/sec
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6/ptodata/1/pubpaa/USO9B_PUBCOMB.pep:*
6/ptodata/1/pubpaa/USO9E_PUBCOMB.pep:*
6/ptodata/1/pubpaa/USO9 NBW PUB.pep:*
6/ptodata/1/pubpaa/USO9 NBW PUB.pep:*
6/ptodata/1/pubpaa/USIOA_PUBCOMB.pep:*
6/ptodata/1/pubpaa/USIOC_PUBCOMB.pep:*
6/ptodata/1/pubpaa/USIOC_PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                         501834
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                         1465611 seqs, 345679903 residues
                                                                                                                                                                                                                                                                                                                                                                                                Listing first 45 summaries
                                                             OM protein - protein search, using sw model
                                                                                                                                                                                                                          Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                100%
                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 08
Maximum Match 10
                                                                                                                                                 US-10-792-311-4
                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0 Maximum DB seq length: 66
                                                                                                                                                                                                             BLOSUM62
                                                                                           June
                                                                                                                                                                   Perfect score:
                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                           Searched:
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Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

					COTTURNION	•
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Result		Query	Query			
No.	Score	Match	Length	DB	נו	Description
-	313	100.0	99	6	US-09-816-989A-4	Sequence 4, Appli
7	313	100.0	99	17	US-10-792-311-4	Sequence 4, Appli
e	198	63.3	26	σ	US-09-816-989A-3	Sequence 3, Appli
4	198	63.3	26	17	US-10-792-311-3	Sequence 3, Appli
S	120.5	38.5	45	σ	US-09-816-989A-2	Sequence 2, Appli
9	120.5	38.5	45	17	US-10-792-311-2	Sequence 2, Appli
7	109.5	35.0	63	16	US-10-667-004-20	Sequence 20, Appl
60	105.5	33.7	35	0	US-09-816-989A-1	Sequence 1, Appli
0	105.5	33.7	35	17	US-10-792-311-1	Sequence 1, Appli
10	97.5	31.2	49	16	US-10-667-004-17	Sequence 17, Appl
11	89.5	28.6	9	15	US-10-390-472-16	Sequence 16, Appl
12	84	26.8	28	15	US-10-424-599-278231	Seguence 278231,
13	84	26.8	99	16	US-10-240-430-7	Sequence 7, Appli

61 EAAYEA 66 ||||||

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Sequence 8, Appli Sequence 17, Appl Sequence 21, Appl Sequence 21, Appl Sequence 19453, Sequence 185175, Sequence 185175, Sequence 185175, Sequence 238129, Sequence 248601, Sequence 248601, Sequence 201428, Sequence 202437, Sequence 182635, Sequence 182635, Sequence 214919, Sequence 162476, Sequence 162476, Sequence 162476, Sequence 162476, Sequence 162476, Sequence 162476, Sequence 233, Appli Sequence 150089, Sequence 150089,	
16 US-10-240-430-8 15 US-10-390-472-17 14 US-10-249-567-17 15 US-10-424-599-271000 16 US-10-424-599-191453 15 US-10-424-599-191453 15 US-10-424-599-191453 15 US-10-424-599-191453 16 US-10-424-599-185175 15 US-10-424-599-239429 15 US-10-424-599-239429 15 US-10-424-599-248601 15 US-10-424-599-248601 15 US-10-424-599-201428 15 US-10-424-599-201428 15 US-10-424-599-201439 16 US-10-424-599-280398 16 US-10-424-599-280398 17 US-10-424-599-280398 18 US-10-424-599-280398 19 US-10-424-599-280398 19 US-10-424-599-280398 19 US-10-424-599-280398 19 US-10-437-963-1150089 19 US-10-424-599-218773	4 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
7 7 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	
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4 1 1 1 1 1 1 2 2 2 2 2 2 2 2 2 2 2 2 2	

### ALIGNMENTS

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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: GA, ALEXANDER

APPLICANT: GA, ALEXANDER

TITLE OF INVENTION: AND FOR THERABEUTIC USE

FILE REFERENCE: 2609/60807-A-PCT-US

CURRENT APPLICATION NUMBER: US/09/816,989A

CURRENT APPLICATION NUMBER: PCT/US99/22402

FRIOR FILING DATE: 1998-09-25

FRIOR FILING DATE: 1998-09-24

NUMBER OF SEQ ID NOS: 7

SOSTWARE: PATCHIN PATESION 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 313; DB 9; Best Local Similarity 100.0%; Pred. No. 6.1e-22; Matches 66; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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Sequence 2, Application US/09816989A
Factor No. US20020115103A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TILLS OF INVENTION:
TITLE OF INVENTION:
FILE REPERENCE: 2609/60807-A-PCT-US
FILE REPERENCE: 2609/60807-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lis, Doris
TITLE OF INVENTION: AND FOR THERAPED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKE
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKE
FILE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/10/792,311
CURRENT APPLICATION NUMBER: US/09/816,989
PRIOR PILING DATE: 2001-03-23
PRIOR PILING DATE: 2001-03-25
PRIOR PILING DATE: 1998-09-25
PRIOR PILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 3
LENGTH: 56
                                                                                 1 AKKYAKKEKAY--AKKAB-KAAK--KAEAKAY-KAABAKKK----AEAKYKAEAAKAAAK 50
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                                      1 AKKYAKEKAYAKAKKAEAKAAKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKAAAK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-10-792-311-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 198; DB 17;
Pred. No. 1.9e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 63.3%; Score 198; DB Best Local Similarity 80.3%; Pred. No. 1.9e Matches 53; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/10792311
Publication No. US20050038233A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                                                                                                         61 EAAYEA 66
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US-09-816-989A-2
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US-10-792-311-3
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                                                                                                                                                                      Sequence 4, Application US/10792311

Sequence 4, Application US/10792311

Publication No. US20050038233A1

GENERAL INFORMATION:

APPLICANT: Gad, Alexander

APPLICANT: Gad, Alexander

TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK

TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK

TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK

TITLE OF INVENTION: AND FOR THERAPEUTIC USE

FILE REFRENCE: 2060-00-2

CURRENT FILING DATE: 2004-03-02

PRIOR PILING DATE: 1098-09-25

PRIOR PILING DATE: 1998-09-25

PRIOR PILING DATE: 1998-09-24

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PATENTIN VEYSION 3.1

SEG ID NO 4

LENGTH: 66
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TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE REPRENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 1998-09-25
PRIOR FILING DATE: 1999-09-25
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-10-792-311-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09816989A
Patent No. US20020115103A1
GENERAL INFORMATION:
APPLICANT: Gad, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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Best Local Similarity 80.3
Matches 53; Conservative
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61 EAAYEA 66
61 EAAYEA 66
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US-09-816-989A-3
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APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKE
TITLE OF INVENTION: ADD FOR THERADEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID MOS: 7
SOFTWARE: PATCHIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKE
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT PELING DATE: 2004-03-02
PRIOR APPLICATION NUMBER: US/9/816,989
PRIOR FILING DATE: 2001-03-23
PRIOR FILING DATE: 2001-03-32
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1998-09-24
PRIOR FILING DATE: 1999-09-24
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                                                                                                                                                                                     1 AKKYAKKEKAYAKAKKABAKAAKKAKAEAKKYAKAKAEKKEYAAAEAKYKAEAAKAAAK 60
                                                                                                                                                                                                                                      ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-1
                                                                                                                                    Gaps
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2
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Pred. No. 0.0036;
2; Mismatches 4; Indels 3:
                                                                                 Score 109.5; DB 16; Length
Pred. No. 0.0029;
0; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
; OTHER INFORMATION: Synthetic peptide US-10-667-004-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09816989A
Patent No. US20020115103A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/10792311 Publication No. US20050038233A1 GENERAL INFORMATION:
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illarity 43.9%;
Conservative
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                                                                                 Query Match 35.0%;
Best Local Similarity 56.5%;
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AKKYAKKEKAAKKAYKKEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Gad, Alexander
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nes 29; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EAAYEA 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
APPLICANT: Lis, Dorig
APPLICANTON: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-FCT-US
FILE REFERENCE: 2609/60807-A-FCT-US
FILING DATE: 2004-03-02
PRIOR APPLICATION NUMBER: BO/101,693
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.1
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APPLICANT: INTEL CORPORATION
APPLICANT: INTEL CORPORATION
APPLICANT: GIAN, Selena
APPLICANT: GIAN, Selena
APPLICANT: GIAN, Silena
APPLICANT: SU, Xing
APPLICANT: SU, Xing
APPLICANT: SU, Xing
APPLICANT: SCANNING PROBE MICROSCOPY (SPM)
FILLE OF INVENTION: CONTROLLED ALIGNMENT OF NANO-BARCODES ENCODING SPECIFIC INFORMATI
TITLE OF INVENTION: SCANNING PROBE MICROSCOPY (SPM)
FILLS REFERENCE: INTEL1310-1(P14240X)
CURRENT APPLICATION NUMBER: US/10/667,004
CURRENT FILING DATE: 2003-09-19
PRIOR PAPLICATION NUMBER: US 10/251,152
PRIOR FILING DATE: 2002-09-20
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5;
                                                                                                                                                                  7
        ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38.5%; Score 120.5; DB 17; Length 45; 71.1%; Pred. No. 0.0002; Live 0; Mismatches 6; Indels 7
                                                                                                            Score 120.5; DB 9; Length 45; Pred. No. 0.0002; 0; Mismatches 6; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AKKYAKKAKAKAKKAYKAAKAAKKAAKYEKAAAEKAAAKEAAYEA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 AKKYAKAAKAE--KKEYAAAEAK-----YKAEAAKAAAKEAAYEA 66
                                                                                                                                                                                                                      29 AKKYAKAAKAE--KKEYAAAEAK-----YKAEAAKAAAKEAAYEA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20, Application US/10667004 Publication No. US20040126820A1
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/10792311
Publication No. US20050038233A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                               Query Match 38.5%;
Best Local Similarity 71.1%;
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-667-004-20
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LENGTH: 63
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: About K
APPLICANT: Alou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223) B
CURRENT APPLICANION NUMBER: US/10/424,599
CURRENT APPLICANION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 278231
LENGTH: 58
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ن
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ADDRESSEE: HAMILION, BROOK, SMITH & REYNOLDS, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 84; DB 15; Length 58;
Pred. No. 0.58;
5; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 KKYAKKEKAYAKAKA---EAKAAKKAKAEAKKYAKAAKAEKKE 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 KAAAAKRAAAKAKKAKKAAKKAKKAKKPAKKSPKKAKKPAKK 57
                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AKKYAKKEKAYAKAKKAEAKAAKKAKAEKKYAKAAKAEKKE 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_93266C.l.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               i, DB 15;
0.19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Brock, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: MIT-6008A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/293,284
FILING DATE: 22-AUG-1994
APPLICATION NUMBER: 07/973,326
FILING DATE: 28-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/390,472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 89.5;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
TOPOLOGY: linear
;
MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-390-472-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 278231, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (617) 861-6240
                         STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                       FILING DATE: 17-Mar-2003
CLASSIFICATION: 435
                                                                                               COUNTRY: U.S.A.
ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 60 amino acids
                                                                       STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.6%;
56.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (617) 861-5
INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.8%;
45.2%;
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Best Local Similarity 45.23
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 56.8
Matches 25; Conservative
                                                   CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-424-599-278231
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APPLICANT: INTEL CORPORATION
APPLICANT: SOLENA
APPLICANT: SOLENA
APPLICANT: SOLENA
APPLICANT: SOLENA
APPLICANT: YAWAKAWA, MINEO
TITLE OF INVENTION: CONTROLLED ALIGNMENT OF NANO-BARCODES ENCODING SPECIFIC INFORMATI
TITLE OF INVENTION: SCANNING PROBE MICROSCOPY (SPM)
FILE REFERENCE: INTELL310-1 (P14240X)
CURRENT APPLICATION NUMBER: US/10/667,004
FILE REPRENCE: 107EL1310-1 (P14240X)
CURRENT FILING DATE: 2002-09-19
PRIOR PILING DATE: 2002-09-20
NUMBER OF SEQ ID NOS: 26
SOFFWARE: Patentin version 3.1
SEQ ID NO 17
LENGTH: 49
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                                                                                                                                                                                                                                                                                                                                                                                               ------KAKAAEAAK 29
                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-10-792-311-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 16, Application US/10390472
Publication No. US20040087013A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Holmes, Todd
Zhang, Shuguang
Rich, Alexander
DiPersio, C. Michael
Lockshin, Curtis
Lockshin, Curtis
SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
                                                                                                                                                                                                                                                                                             31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 31.2%; Score 97.5; DB 16; Length 49; 1 Similarity 58.5%; Pred. No. 0.028; 31; Conservative 0; Mismatches 17; Indels
                                                                                                                                                                                                                                            Query Match 33.7%; Score 105.5; DB 17; Length Best Local Similarity 43.9%; Pred. No. 0.0036; Matches 29; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Synthetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17, Application US/10667004 Publication No. US20040126820A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THEREFOR
                       SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 35
                                                                                                                                                                                                                                                                                                                                                                                               1 AKKYAKKEKAAKKAYKKEA
                                                                                                                   ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 31; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                               61 EAAYEA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EAAYEA 35
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US-10-667-004-17
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US-10-390-472-16
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1 KKAKKPAAAAGAKK--AKSPKKAKA----AKPKKAPKSPAKAKAVKPKAAKPKTAKPKA 53
                                                                                                                                                                                                                                                                                                                                                                                               Lockshin, Curtis
INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 KAKKAEAKAAKKAKAEAKKYAKAAKAEKKEYAAAEAKYKA-EAAKAAAKEAA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 26.7%; Score 83.5; DB 15; Length 61; Best Local Similarity 48.1%; Pred. No. 0.68; Matches 25; Conservative 5; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTY 10.5.A.

ZIP: 02173-4799

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/390,472

FILING DATE: 17-Mar-2003

CLASSIFTCATION: 435

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/293,284
FILING DATE: 22-AUG-1994
APPLICATION NUMBER: 07/973,326
FILING DATE: 28-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGIESTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: MIT-600BA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        search completed: June 3, 2005, 11:09:50
Job time: 139 secs
                                                                                                                                                                                                                                                                                                                            Zhang, Shuguang
Rich, Alexander
DiPersio, C. Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: Two Militia Drive
                                                                                                                                                                                                                         Sequence 17, Application US/10390472
Publication No. US20040087013A1
GENERAL INFORMATION:
APPLICANT: Holmes, Todd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 61 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Lexington
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                      63 A 63
                                                                                                     54 Å 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 KYAKKEKAYAKAKKAEAKAAKKAKAEAKKYAKAAKAEKKEYAAAEAKYK-----AEAAK 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KKAKKPAAAAGAKK--AKSPKKAKAKPKKAPKSPAKAKAVKPKAAKPKTAKPKAAKPKK 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 KYAKKEKAYAKAKKAEAKAAKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKAAAKEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence as Application US/10240430
; Sequence B. Application US/10240430
; Publication No. US20040110928A1
; GENERAL INFORMATION:
   APPLICANT: Crisanti, Andrea
; APPLICANT: Esseghir, Selma
; TITLE OF INVENTION: Peptide Conjugates for Drug Delivery
; FILE REFERENCE: GJE-6402
; CURRENT APPLICATION NUMBER: US/10/240,430
; CURRENT FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: UK 0102667.3
; PRIOR PILING DATE: 2001-04-12
; PRIOR PLING DATE: 2001-04-12
; PRIOR PLING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PATENTIN UNICHARIAN STATES
; TYPER PLING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NOS: 14
                                                                                                                                      Sequence 7, Application US/10240430

Publication No. US20040110928A1

GENERAL INFORMATION:
APPLICANT: Crisanti, Andrea
APPLICANT: Essequir, Selma
TITLE OF INVENTION: Peptide Conjugates for Drug Delivery
FILE REFERENCE: GJS-64102
CURRENT APPLICATION NUMBER: US/10/240,430
CURRENT FILING DATE: 2003-04-15
PRIOR APPLICATION NUMBER: UK 0102667.3
PRIOR PILING DATE: 2001-04-12
PRIOR FILING DATE: 2001-04-12
PRIOR FILING DATE: 2001-04-12
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTING DATE: 2000-04-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 16; Length 66;
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SKYLKKKEKKKKKKKKKRTKTKKKKKKK 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 84; DB 16
Pred. No. 0.67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Mismatches
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Best Local Similarity 42.69
Matches 29, Conservative
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ORGANISM: Homo sapiens
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US-10-240-430-8
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59 AAAKKKEF 66
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US-10-240-430-8
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RESULT 2
US-09-816-989A-4
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Matches 6
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117.306 Million cell updates/sec
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Sequence 1, A
Sequence 16,
Sequence 16,
Sequence 16,
Sequence 16,
Sequence 6, A
Sequence 7, A
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                                                                                                                           3, 2005, 10:47:50 ; Search time 42 Seconds
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1. /cgn2_6/ptodatca1/liaa/5A_COMB.pep:*

2. /cgn2_6/ptodatca1/liaa/5B_COMB.pep:*

3. /cgn2_6/ptodatca1/liaa/6A_COMB.pep:*

4. /cgn2_6/ptodatca1/liaa/6B_COMB.pep:*

5. /cgn2_6/ptodatca1/liaa/PCTUS_COMB.pep:*

6. /cgn2_6/ptodatca1/liaa/PCTUS_COMB.pep:*

6. /cgn2_6/ptodatca1/liaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-405-743A-3
US-09-405-743A-3
US-09-405-743A-2
US-09-816-989A-2
US-08-993-008A-5
US-08-993-008A-5
US-08-993-008A-1
US-08-393-284A-1
US-08-898-300-16
US-08-998-300-16
US-08-998-172-6
US-08-995-172-7
US-08-221-050-7
US-08-291-284A-17
US-08-291-284A-17
US-08-291-284A-17
US-08-291-284B-17
US-08-291-284B-17
US-08-291-284B-13
US-08-152-488-13
US-08-152-488-13
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US-08-152-488-13
US-08-152-488-13
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Maximum Match 100%
Listing first 45 summaries
                                                                                      OM protein - protein search, using sw model
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Match Length DB
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Maximum DB seq length: 66
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No.
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Sequence 4, Application US/0981698A

Sequence 4, Application US/0981698A

Sequence 6, Application US/0981698A

Resent No. 6800287

GRNERAL INFORMATION:

APPLICANT: Gad, Alexander

APPLICANT: Lis, Doris

TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKE

TITLE OF INVENTION: AND FOR THERAPEUTIC USE

FILE REPERENCE: 2609/60807-A-PCT-US

CURRENT APPLICATION NUMBER: US/09/816,989A

CURRENT FILING DATE: 1998-09-25

PRIOR FILING DATE: 1998-09-25

PRIOR FILING DATE: 1999-09-24
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                                                                         Sequence
                               Sequence
Sequence
Sequence
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                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09405743A

Patent No. 6514938
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Veda Research and Development Co., Ltd.
ATTLE OF INVENTION: GLATICAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 313; DB 4;
100.0%; Pred. No. 1.2e-23;
tive 0; Mismatches 0;
US-08-303-025-16
US-08-436-03B-4
US-09-411-264-41
US-09-417-264-41
US-08-995-172-20
US-08-460-890A-58
US-08-460-971A-58
US-08-460-971A-58
US-08-460-971A-60
US-08-460-971A-60
US-08-460-971A-60
US-08-460-971A-60
US-08-460-971A-60
US-08-167-641C-60
US-08-167-641C-60
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US-08-167-641C-60
US-08-167-641C-60
US-08-167-641C-60
US-08-162-0410-60
US-08-162-0410-60
US-08-162-0410-60
US-08-162-0410-60
US-08-163-1711-30
US-08-584-043A-131
US-08-1171-30
US-08-130-7038-1
                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 100.
66; Conservative
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   82
81.5
81.5
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APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKE
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REPERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23
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                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-3
                                                                                                                                                                                                                                                                                                           Gaps
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US-09-405-743A-2
                                                                                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
TILE REPERENCE: 60807-A
CURRENT APPLICATION WHERE: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 38.5%; Score 120.5; DB 4; Length 45; Local Similarity 71.1%; Pred. No. 2.5e-05; les 32; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                         Length 56;
                                                                                                                                                                                                                                                                                                           1; Indels
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                                                                                                                                                                                                                                                       Score 198; DB 4;
Pred. No. 1.1e-12;
2; Mismatches 1
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PRIOR FILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFWARE: Patentin version 3.1
LENGTH: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Faquence 2, Application US/09405743A; Patent No. 6514938; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09816989A
Patent No. 6800287
PREMERAL INFORMATION:
APPLICANT: Gad, Alexander
                            SOFTWARE: PatentIn version 3.1
                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                       Query Match 63.3%;
Best Local Similarity 80.3%;
Matches 53; Conservative
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ORGANISM: Artificial Sequence
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  NUMBER OF SEQ ID NOS:
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51 EAAYEA 56
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US-09-405-743A-2
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                                                 SEQ ID NO 3
LENGTH: 56
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LENGTH: 45
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APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
APPLICANT: Lis, Dorit WEBER
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/660807-AP-PCT-US
CURRENT APPLICATION NUMBER: US/09/816, 989A
CURRENT FILING DATE: 2001-03-23
                                                                                                                                                                                                                                                                                                                                                                                          1 AKKYAKKEKAYAKAKKAEAKAAKKAKAKAKAYAKAAKAEKKEYAAAEKKYKAEAAKAAKK 60
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                                                                                                                                                                          ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-4
                                                                                                                                                                                                                                                                                                                                                        1 AKKYAKKEKAYAKAKKAEAKAAKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKAAAK
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TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
LENGTH: 56
                                                                                                                                                                                                                                                    Length 66;
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                                                                                                                                                                                                                                                    Query Match

100.0%; Score 313; DB 4;

Best Local Similarity 100.0%; Pred. No. 1.2e-23;

Matches 66; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR FILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: ECT/US99/22402
PRIOR FILING DATE: 1999-09-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/09405743A Patent No. 6514938 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/09816989A
Patent No. 6800287
                          SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                        ORGANISM: Artificial Sequence
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 EAAYEA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EAAYEA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EAAYEA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EAAYEA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
US-09-405-743A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-816-989A-3
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                                                                                                   TYPE: PRT
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Sequence 1, Application US/09405743A Patent No. 6514938 GENERAL INFORMATION:
                               Sequence 5, Application US/08993008A Patent No. 6153596 GENERAL INFORMATION: APPLICANT: Liotta, Dennis C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 33
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SS: not relevant not relevant
                                                                                               Liotta, Dennis C.
Petros, John A.
                                                                                                                APPLICANT: Petros, John A. APPLICANT: Wey, Shlow-Jyi APPLICANT: Karr, Joan F. APPLICANT: Pohl, Jan TITLE OF INVENTION: POLYCAL NUMBER OF SEQUENCES: 6 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 48 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 303-499-8089
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                      Boulder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                               ZIP: 80303
                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ANTI-SENSE:
US-08-993-008A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-405-743A-1
                   JS-08-993-008A-5
                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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LENGTH: 35
TYPE: PRT
                                                                                                                                                                                                                                                                                   STREET:
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Best Local
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                                                                                                                                                              ä
                                      FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-2
                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 КАУАКАК-КАЕАКААККАКАЕАККУАКА-АКАЕККЕУАААЕАКУКАЕА-АКАААК 60
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37.5%; Score 117.5; DB 3; Length 56;
Best Local Similarity 65.5%; Pred. No. 6e-05;
Matches 36; Conservative 5; Mismatches 11; Indels
                                                                                                                Query Match
38.5%; Score 120.5; DB 4; Length 45;
Best Local Similarity . 71.1%; Pred. No. 2.5e-05;
Matches 32; Conservative 0; Mismatches 6; Indels '
                                                                                                                                                                                                       29 AKKYAKAAKAE--KKEYAAAEAK----YKAEAAKAAAKEAAYEA 66
                                                                                                                                                                                                                                           1 AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAKEAAYEA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,008A
FILING DATE: 18-DEC-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032,436
FILING DATE: 18-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: SULLIVAN, SALLY AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .5;
. 6e-05;
11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polycationic Oligomers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                         US-08-993-008A-6
; Sequence 6, Application US/08993008A
; Patent No. 6153596
                                                                                                                                                                                                                                                                                                                                                                 Patent No. 6153596
GENERAL INFORMATION:
APPLICANT: Lictta, Dennis C.
APPLICANT: Petros, John A.
APPLICANT: Wey, Shlow-Jyi
APPLICANT: KATT, Joan F.
APPLICANT: Petros, Joan F.
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not relevant
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TELEPHONE: 303-499-8080
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 56 amino acids
TYPE: amino acid
STRANDEDNESS: not relev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         303-499-8089
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: not
MOLECULE TYPE: 1
HYPOTHETICAL: N
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US-08-993-008A-6
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TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,008A
FLING DATE: 18-DEC-1997
PLING APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
RAPPLICATION NUMBER: US 60/032,436
FILING DATE: 18-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: SUllivan, Sally A.
REGISTRATION NUMBER: 32,0649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34.2%; Score 107; DB 3; 64.6%; Pred. No. 0.00053; tive 5; Mismatches 10;
                                                                              3: Greenlee, Winner and Sullivan
5370 Manhattan Circle, Suite 201
Polycationic Oligomers
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Gaps
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APPLICANT: Lockshin, Curtis
TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
NUMBER OF SEQUENCES: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 KKYAKKEKAYAKAKA---EAKAAKKAKAEAKKYAKAAKAEKKE 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Batentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,849
FILING DATE:
CLASSIFICATION NUMBER: 07/973,326
FILING DATE: 28 DECEMBER 1992
FILING DATE: 28 DECEMBER 1992
ATTORNEY AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REGISTRATION NUMBER: 22,592
REGISTRATION NUMBER: MIT-6008
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.C.:
COUNTRY: U.C.:
ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/293,284A
TILING DATE: 2-Aug-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILION, BROOK, SMITH & REYNOLDS, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 16, Application US/08293284A Patent No. 5955343 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Holmes, Todd
APPLICANT: Zhang, Shuguang
APPLICANT: Rich, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 56.8
Matches 25; Conservative
                          Lexington
Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                          CITY: Lexington STATE: Massachu COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Lexington
STATE: Massachu
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-293-284A-16
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APPLICANT: Gad, Alexander
APPLICANT: Lia, Doria
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
TITLE OF INVENTION: UNMER: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: 60/101, 693
PRIOR PAPLICATION NUMBER: 60/101, 693
PRIOR PAPLICATION NUMBER: PCT/US99/22402
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR PLING DATE: 1999-09-25
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PALENTIN VETSION 3.1
SEQ ID NOS: 7
SOFTWARE: PALENTIN VETSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AKKYAKKEKAYAKAKKAEAKAAKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKAAAK 60
                                                                                                                                                                                                                                                                                                 , OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-1
                                                                                                                                                                                                                                                  1 AKKYAKKEKAYAKAKKAEAKAAKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKAAAK
                                                                                                                                                                                                 4; Indels 31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels 31; Gaps
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TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
TITLE OF INVENTION: THEREFOR
TITLE OF INVENTION: 64
CORRESPONDENCE ADDRESS:
                                                 SYNTHETIC
                                                                                                                                          33.7%; Score 105.5; DB 4; Length 35; 43.9%; Pred. No. 0.00053; tive 2; Mismatches 4; Indels 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 33.7%; Score 105.5; DB 4; Length 35; Best Local Similarity 43.9%; Pred. No. 0.00053;
                                               OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
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Patent No. 5670483
GENERAL INFORMATION:
APPLICANT: Zhang, Shuguang
APPLICANT: Lockshin, Curtis
APPLICANT: Rich, Alexander
APPLICANT: Holmes, Todd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09816989A Patent No. 6800287
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                               Query Match
Best Local Similarity 43.94
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29; Conservative
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US-09-816-989A-1
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22,592
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INFORMATION FOR SEQ ID NO: 16:
                                                                                                    28.6%;
56.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Brook, David E.
REGISTRATION NUMBER: 22,
REFERENCE/DOCKET NUMBER:
                                                                                          Query Match 28.6
Best Local Similarity 56.8
Matches 25; Conservative
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Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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US-08-824-513-16
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US-08-898-300-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 28.6%; Score 89.5; DB 2; Length 60; Best Local Similarity 56.8%; Pred. No. 0.032; Matches 25; Conservative 2; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 16, Application US/08898300
; Patent No. 6548630
; GENERAL INFORMATION:
   APPLICANT: Zhang, Shuguang
   APPLICANT: Rich, Alexander
   APPLICANT: Holmes, Todd
   TILLE OF INVENTION: STEALE MACROSCOPIC MEMBRANES FORMED
   TILLE OF INVENTION: THEREFOR
   TITLE OF INVENTION: THER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 KKYAKKEKAYAKAKKA---EAKAAKKAKAEAKKYAKAAKAEKKE 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 KAAAAKKAAAKKAKKAKKAAKKAAKKAKKPAKKSPKKAKKPAKK 57
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CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02173-479
ZIP: 02173-479
COMPUTER: EABABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/898,300
FILING DATE: 22 JULY 1997
CLASSIFICATION: 514
PRIOR APPLICATION BATA:
APPLICATION NUMBER: 08/346,849
FILING DATE: 30 NOVENBER 1994
PRIOR APPLICATION NUMBER: 07/973,326
FILING DATE: 28 DECEMBER 1992
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 21,592
ATTORNEY/AGENT INFORMATION:
NAME: BLOOK, DAVIG E.
REGISTRATION NUMBER: 22,592
REGISTRATION NUMBER: 22,592
REGISTRATION NUMBER: 21,592
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 861-9540
INFORMATION POR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
FEMILE FOR A MILLO ACIDS
FEMILE FOR ACIDS
FEMILE FOR A MILLO ACIDS
FEMILE FOR ACIDS
FEMILE FO
                                                                                    NAME: Brook, David B.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: MIT-6008A
TELEPHONE: (617) 861-6240
TELEPHONE: (617) 861-9540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 amino acids
TYPE: amino acids
TOPOLOGY: linear
                                               INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-293-284A-16
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MOLECULE TYPE: protein
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Gaps
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SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
THEREFOR
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Score 89.5; DB 4; Length 60;
Pred. No. 0.032;
2; Mismatches 14; Indels
                                                                                                 2 KKYAKKEKAYAKAKA---EAKAAKKAKAEAKKYAKAAKAEKKE 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 KKYAKKEKAYAKAKKA---EAKAAKKAKAEAKKYAKAAKAEKKE 42
                                                                                                                                               14 KAAAAKRKAAKKAKKPKKKAAKKAKKPAKKSPKKAKKPAKK 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: Two Militia Drive
CITY: Learington
STATE: Massachusetts
COUNTRY: U.S.A.
ZATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: FORM:
MEDIUM TYPE: FORM:
MEDIUM TYPE: PLOPPY disk
COMPUTER: IBM PC COMPATIBLE
OPFRATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/824,513
FILING APPLICATION HATA:
APPLICATION NUMBER: 26, 1997
FILING APPLICATION NUMBER: 20, 1998
PRIOR APPLICATION NUMBER: 00/293,284
FILING DATE: AUGUST 22, 1998
PRIOR APPLICATION NUMBER: 07/973,326
FILING DATE: 28 DECEMBER 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (781) 861-6240
                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Zhang, Shuguang
APPLICANT: Rich, Alexander
APPLICANT: DiPersio, C. Michael
APPLICANT: Lockshin, Curtis
TITLE OF INVENTION: SELF-ASSEMBLY
TITLE OF INVENTION: TERREFOR
TITLE OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                Sequence 16, Application US/08824513
Patent No. 6800481
GENERAL INFORMATION:
APPLICANT: Holmes, Todd
APPLICANT: Zhang, Shuguang
APPLICANT: Rich, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
US-08-995-172-6
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Sequence 6, Application US/08995172B
Patent No. 6218112
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
THIS OF INVENTION:
THIS OF INVENTION: Optimization of Gene Delivery and Gene Delivery Systems
FILE REPRENCE: CACCO026
CURRENT APPLICATION NUMBER: US/08/995,172B
CURRENT APPLICATION NUMBER: US/08/995,172B
CURRENT APPLICATION NUMBER: US/08/995,172B
CURRENT APPLICATION NUMBER: US/033,908
EARLIER FILING DATE: 1996-12-23
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 61
TYPE: PRT
ORGANISM: Artificial Sequence
FRAURE INFORMATION: Description of Artificial Sequence: Peptide
US-08-995-172-6
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Query Match 26.8%; Score 84; DB 3; Length 61; Best Local Similarity 45.8%; Pred. No. 0.11; Matches 27; Conservative 8; Mismatches 22; Indels

7

2; Gaps

Search completed: June 3, 2005, 10:58:21 Job time: 43 secs

```
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

June 3, 2005, 11:06:37 ; Search time 38 Seconds (without alignments) 194.966 Million cell updates/sec

US-10-792-311-5 366 1 AKKYAKKEKAYAKKAEKAAK......BAKYKAEAAKAAAKEAAYEA 77 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

24506 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 77

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

•• Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Description	hypothetical prote	-44	protamine phi-3.3	protamine phi-3.2	nonhistone chromos	_	histone H1.4 - rab	gene 14 protein -	gene 4.3 protein -	hypothetical prote	protein YDL085c-a	υ				ribosomal protein	probable histone H	myosin heavy chain	hypothetical prote	ribosomal protein	antifreeze protein	hypothetical prote	archaeal histone -	archaeal histone -	M protein precurso	collagen alpha 1(X	alpha-myosin heavy	pollen coat protei	histone HMtA2 - Me
ID	T30977	S04941	S10545	S10544	NSTR6	G83572	A02579	S58143	807510	996695	S78710	A87439	S58762	S58760	S78292	S78240	T07842	S61536	T22415	S70831	A05163	A95330	A64321	D64416	860851	A56371	146866	T14467	G69093
qth DB	62 2	45 2	45 2																								7		68 2
\$ Query Match Length	22.4	20.8		19.7	19.4	17.6	17.2	16.4	16.4	16.3	16.1			15.8	15.7	15.7	15.6	15.6	15.6	15.2	15.0	15.0	15.0	15.0	14.9	14.8	14.8	14.8	14.8
Score	. 60	94 .	73	72	71	64.5	63	9	09	59.5	59	28	28	28	•	57.5	57	57	57	55.5	55	55	52	55	54.5	54	54	54	54
Result No.		C)	٣	4	2	9	7	æ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23		25	26	27	28	29

ä

Gaps 4.

Ouery Match 20.8%; Score 76; DB 2; Length 45; Best Local Similarity 44.4%; Pred. No. 11; Matches 20; Conservative 8; Mismatches 13; Indels

M protein precurso	troponin T, cardia	M protein precurso	hypothetical prote	mercuric reductase	hypothetical prote	hypothetical prote	tandem repeat pept	probable motility	ribosomal protein	hypothetical prote	myosin catalytic l	isoprenylated prot	M-like protein pre	antifreeze protein	probable ribosomal
860836	S48790	S60844	F64031	A86729	F82154	AG3440	PT0028	F71847	A64163	AH1358	S01945	T06397	S62073	FDF18G	T05930
~	7	7	~	7	7	7	7	7	7	~	N	~	7	-	7
74	72	72	73	99	67	70	44	54	61	69	52	74	75	40	74
14.8	14.6	14.6	14.6	14.5	14.5	14.5	14.3	14.3	14.2	14.2	14.1	14.1	14.1	13.9	13.9
54	53.5	53.5	53.5	53	53	23	52.5	52.5	52	52	51.5	51.5	51.5	51	51
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

RESULT 1 T30977
hypothetical protein COIB10.5 - Caenorhabditis elegans C.Species: Caenorhabditis elegans C.Date: 22-0ct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
R. Blanchard, M.; Bradshaw, H. submitted to the RWBL Data Library, August 1999 A. Bescription: The sequence of C. elegans cosmid ColB10 A. Reference number: Z20949
A;Accession: T30977 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Mesidues: 1-62 < BLA> A;Acresieues: UNIPROT:Q17536; EMBL:U58757; PIDN:AAC47916.1
A;Experimental source: strain Bristol N2 C;Genetics: A;Map position: IV A;Introns: 27/3; 61/3 A;Note: C01B10.5
Query Match 22.4%; Score 82; DB 2; Length 62; Best Local Similarity 43.6%; Pred. No. 5.1; Matches 24; Conservative 5; Mismatches 24; Indels 2; Gaps 1;
OY 1 AKKYAKKEKAYAKKAEKAAKKABAKAYKAABAKKKAKABAKKYAKAAKAEKKE 53
Db 7 AKKVAKTKKVAAKPKAPKVKKIQASPKKAAAPKAKKPVKKAAAKKSPAKKAAPKK 61
RESULT 2 S04941 protamine phi-3.1 - California mussel N.Alternate names: protamine PL-IV.1 C;Becies: Wytilus californianus (California mussel) C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004 C;Accession: S04941
R.Ausio, J.; McParland, R. Bur. J. Biochem. 182, 569-576, 1989 A.Title: Sequence and characterization of the sperm-specific protein phi3 from Mytilus of A.Reference numbers: 804941; MUID:89325302; PMID:2666130
A; Molecule type: protein A; Molecule type: protein A; Residues: 1-45 < AUS> A; Cross-references: UNIPROT: P11860 A; Note: 6-Thr, 17-Thr, and 18-Thr was also found C; Superfamily: histone H1
Civeywords: Day Dilighing; Indicates

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à 셤 protamine phi-3.3 - California mussel

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C,Accession: A02579 8.D. J. Stall, S.C.; Cole, R.D. J. Biol. Chem. 246, 7175-7190, 1971 A.F.Itle: Amino acid sequence and sequence variability of the amino-terminal regions of l). A;Reference number: A02578; MUID:72068710; PMID:5167020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M.J.; Bri
K.; Lim,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathoc A,Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:Q915V8; GB:AE004494; GB:AE004091; NID:g9946446; PIDN:AAG03968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleosome; nucleus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30S ribosomal protein S21 PA0579 [imported] - Pseudomonas aeruginosa (strain PAO1) C;Species: Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Species: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004 R;Stowsr, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.. i. Lory, S.; Olson, M.V.
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                                                                                                                                                                                                                                                                                                                                          13 KKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAKAKAEKKEYAAAEAKYKAEAAKAAKE 72
                                                                                                                                                                                                                                                                                                                                                                          4 KSATKGDEPARRSARLSARPVPKPAAKPKKAAAPKKAAAAPKKAAAENGDAKAEAKVQAAGD 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A02579
histone Hl.4 - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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C;Keywords: acetylated amino end; chromosomal protein; DNA binding;
F;1/Modified site: acetylated amino end (Ser) #status experimental
F;37/Binding site: phosphate (Ser) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 KAYAKKAEKAAKKAEAKAYK-----AAEAKKKAKAEAKKYAKAAKAEKK 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 17.6%; Score 64.5; DB 2; Length 7: 1 Similarity 30.6%; Pred. No. 1.1e+02; 15; Conservative 12; Mismatches 17; Indels
                                                                                                                                                                                                                   Score 71; DB 1; Length 69;
Pred. No. 35;
5; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Cross-references: UNIPROT: P02252
R;Langan, T.A.; Rall, S.C.; Cole, R.D.
J. Biol. Chem. 246, 1942-1944, 1971
A;Reference number: A37504; MUID:71134818; PMID:5547708
A;Contents: annotation
A;Residues: 1-69 <WAT>
A;Cross-references: UNIPROT:P02315
A;Experimental source: testis
A;Note: this protein was formerly called histone T
C;Superfamily: nonhistone chromosomal protein HWG-17
C;Keywords: chromosomal protein; DNA binding; nucleus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Genetics:
A;Gene: rpsU; PA0579
C;Superfamily: Bscherichia coli ribosomal protein S21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Experimental source: strain PAO1
                                                                                                                                                                                                                Query Match
Best Local Similarity 36.9%;
Matches 24; Conservative
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A;Residues: 1-73 <RAL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 AAYEA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 GAGNA 68
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A; Residues: 1-71 <STO>
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Matches
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RyAccesion: A02653
RyAccesion: A02653
Bur. J. Biochem. 95, 193-202, 1979
Aritile: The complete amino-acid sequence of a trout-testis non-histone protein, H6, loc A; Reference number: A02653; MUID:79213375; PMID:456349
A; Accession: A02653
A; Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                             C;Accession: S10545
R;Ausio, J; McParland, R.
Bur. J. Blochem. 182, 569-576, 1989
A;Title: Sequence and characterization of the sperm-specific protein phi3 from Mytilus A;Accession: S10545
A;Accession: S10545
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(Species: Mytilus californiamus (California mussel)

(Space) 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004

(Spacession: S10544

R.Ausio, J.; McParland, R.

Eur. J. Blochem. 182, 569-576, 1989

A;Telle: Sequence and characterization of the sperm-specific protein phi3 from Mytilus

A;Reference number: S04941; MUID:89325302; PMID:2666130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ä
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                                                                                                                                                                                                                                                                           N,Alternate names: protamine PL-IV.3
C;Species: Mytilus californianus (California mussel)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
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NiAlternate names: histone T
C:Species: Oncorhynchus mykiss (rainbow trout)
C:Species: 30-Sep-1979 #sequence_revision 08-Oct-1981 #text_change 09-Jul-2004
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                                                                     1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAK 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 AKRSPRKKKAAVKK----SSKSKAKKPKSPKKKKAAKKPARKAAK 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAK 45
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protamine phi-3.2 - California mussel

A,Molecule type: protein
A,Residues: 1-45 AAUS>
A,Cross-references: UNIPROT:P11860
C;Superfamily: histone H1
C;Keywords: DNA binding; nucleus

A; Accession: S10544

ilarity 42.2%; Conservative

Best Local Similarity Matches 19; Conserv

RESULT 5

Query Match

Score 73; DB Pred. No. 18; 9; Mismatches

19.9%;

Query Match Best Local Similarity

Conservative

19;

Matches

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A;Molecule type: protein A;Residues: 1-45 <AUS> A;Cross-references: UNIPROT:P11860

C; Superfamily: histone H1 C; Keywords: DNA binding; nucleus

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C;Species: Bacillus subtilis
C;Accession: G69966
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berterk
C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallert
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.;
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueell,
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parrxo, V.; Pohl, T.M.; Portetelle,
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Rocse, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seror,
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Toganot, N.; Yoshida, K.;
Y, Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yasukoto,
A;Authors: Yoshikawa, H.F.; Zumetein, B.; Yoshikawa, H.; Danchin, A.
A;Title: The complete geneme sequence of the Gram-positive bacterium Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:P54568; GB:Z99116; GB:AL009126; NID:g2634723; PIDN:CAB14295.1
A;Experimental source: strain 168
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevision 15-Jan-1999 #text_change 15-Jan-1999
C;Accession: S78710
R;Wambutt, R.; Wedler, H.; Wedler, E.; Scharfe, M.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S67608
A;Reference number: S67708
A;Reference number: S78710
A;Status: preliminary
A;Molecule type: DNA
A;Reference DNA
A;Residues: 1-68 < WAM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.3%; Score 59.5; DB 2; Length 74; 38.5%; Pred. No. 2.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: A69580; MUID: 98044033; PMID: 9384377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein YDL085c-a - yeast (Saccharomyces cerevisiae)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Experimental source: strain S288C C,Genetics:
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A;Title: The complete nucleotide sequence and functional organization of Bacillus subtil A;Reference number: Z22137; MUID:98094274; PMID:9434185
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C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene 14 protein - phage SPP1
C;Species: phage SPP1
C;Date: 13-Jan-1996 #Bequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C;Accession: SSB43; T42284
R;Becker, B.; Gassel, M.; Tavares, P.; Lurz, R.; Alonso, J.C.
submitted to the EMBL Data Library, July 1995
A;Description: Head morphogenesis of the Bacillus subtilis bacteriophage SPP1.
                                                                                                                              68
                                                                                                                                                                                       61
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C:Species: phage T3
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: 807510
C:Accession: 807510
J. Mol. Biol. 210, 687-701, 1989
A;Title: Sequence of bacteriophage T3 DNA from gene 2.5 through gene 9.
A;Accession: 807510
                                                                                                                              9 KAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAABAKYKAEAAKA
                                                                                                                                                                                       2 EAPAETAAPAAKSPATPVKKARKKKSAGAAKRKASGPPVSELITKAVAASKERSGVSLA
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                                                               33; Indels
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Pred. No. 1.9e+02;
7; Mismatches 20;
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Pred. No. 2.2e+02;
         Score 63; DB 2; I
Pred. No. 1.4e+02;
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A,Residues: 1-58 <ALO>
A,Cross-references: BMBL:X97918; PIDN:CAA66545.1
                                                                  21; Conservative 11; Mismatches
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C,Superfamily: phage T7 gene 4.3 protein
17.2%;
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Best Local Similarity 39.6%;
Matches 19; Conservative
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Best Local Similarity 35.4%;
Matches 17; Conservative
Query Match
Best Local Similarity
Matches 21, Conserv
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ALKKA 66
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A; Residues: 1-70 <BEC>
                                                                                                                                                                                                                                                   69 AAKEA 73
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A; Residues: 1-58 <BEC>
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A,Cross-references: UNIPROT:P41787; EMBL:U20491; NID:g665949; PIDN:AAA87001.1; PID:g66599: C,Superfamily: Bscherichia coli ribosomal protein S20
C;Keywords: protein biosynthesis; ribosome; RNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ribosomal protein L32', chloroplast - Odontella sinensis chloroplast C;Species: chloroplast Odontella sinensis C;Species: chloroplast Odontella sinensis C;Date: 17-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 20-Jun-2000 C;Accession: S78292 B;Scobe, B.; Schaffran, I.; Kroth-Pancic, P.; Freier, U. R;Kowallik, K.V.; Stoebe, B.; Schaffran, I.; Kroth-Pancic, P.; Freier, U. Plant Mol. Biol. Rep. 13, 336-342, 1995 A;Title: The Chloroplast Genome of a chlorophyll a+c- containing Alga, Odontella sinensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Cross-references: EMBL:Z67753; NID:g1185127; PIDN:CAA91665.1; PID:g1185182
A,Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Reference number: S78238
A;Accession: S78292
A;Residues: 1-54 <KOW>
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                                                                                                                                   Query Match 15.8%; Score 58; DB 2; Length 72; Best Local Similarity 39.0%; Pred. No. 3.2e+02; Matches 16; Conservative 6; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                              28 KAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Gene: rp132,
A,Genome: chloroplast
C,Superfamily: rice chloroplast ribosomal protein L32
C,Keywords: chloroplast; protein biosynthesis; ribosome
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Pred. No. 2.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAK 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     completed: June 3, 2005, 11:16:14
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Best Local Similarity 45.5%;
Matches 15; Conservative
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Job time : 39 secs
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R;Nemec, A.; Haywood-Farmer, A.; Mackie, G.A.

Biochim. Biophys. Acta 1263, 154-158, 1995

A;Title: Conserved amino acid residues in the primary structure of ribosomal protein S26

A;Accession: S58760; MUD:95367591; PMID:7640306

A;Accession: S58760

A;Molecule type: DNA

A;Residues: 1-72 <NEM>
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C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S58762; S71843
Biochim. Biophys. Acta 1263, 154-158, 1995 A.A.
Biochim. Biophys. Acta 1263, 154-158, 1995 A.A.
A;Title: Conserved amino acid residues in the primary structure of ribosomal protein S20
A;Accession: S58762
                               C;Accession: A87439
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. R;Nierman, W.T.; DeBby, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4135-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:Q9A834; GB:AE005673; NID:g13422913; PIDN:AAK23509.1; GSPDB:
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C; Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
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ribosomal protein S20 - Salmonella typhimurium (fragment)
C;Species: Salmonella typhimurium
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 09-Jul-2004
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-63, "R', 65-72 <MAC>
A;Cross-references: EMBL: U20493; NID:g665953; PIDN:AAA86999.1; PID:g665954
C;Superfamily: Escherichia coll ribosomel protein S20
C;Keywords: protein biosynthesis; ribosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 15.8%; Score 58; DB 2; Length 58; Best Local Similarity 36.8%; Pred. No. 2.7e+02; Matches 14; Conservative 9; Mismatches 15; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ribosomal protein S20 - Klebsiella pneumoniae (fragment)
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Local Similarity 39.0%; Pred. No. 3.2e+02;
les 16; Conservative 6; Mismatches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-72 < NEM>
A; Cross-references: UNIPROT: P45601; EMBL: U20493
R; Mackie, G.A.
submitted to the EMBL Data Library, January 1995
A; Reference number: S71843
                                                                                                                                                                                                                                                                          A; Accession: A87439
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-58 <STO>
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A;Gene: CC1530
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083897 coxiella bu QR3188 chromobacte QR408 plasmodium QB9408 paramecium QB9459 paramecium QB1598 paradomonas Q7150 pseudomonas Q7150 cattus norv Q81410 cattus norv Q81412 xenopus lae Q7126 rattus norv Q81412 xenopus lae Q7126 plasmodium Q73994 bacallus ce

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Trypanosoma brucei gambiense.
Eukaryotea; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBL_TaxID=31285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Trypanosoma cruzi.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=8956492; PubMed=2475776; DOI=10.1016/0166-6851(89)90115-1; Lafaille J.J., Linss J., Krieger M.A., Souto-Padron T., de Souza W., Caddenberg S.; Souto-Padron T., de Souza W., Structure and expression of two Trypanosoma cruzi genes encoding antigenic proteins bearing repetitive epitopes."; Mol. Blochem. Parasicol. 35:127-136(1989).

EMBL; J04016; AA30177.1; -...
InterPro; IPR009761; CRA_rpt. Z.
PFam; PF07046; CRA_rpt. Z.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel..01, Created)
01-NOV-1996 (TrEMBLrel..01, Last sequence update)
01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
Cytoplasmic repetitive antigen (CRA) protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 AA; 7208 MW; ED6CF031B3DE7D1F CRC64;
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Last annotation update)
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                      083AG7
07NS18
08NS18
08MS6
06BGR3
06BGR3
07S21
PSEAE
RS21
PSEAE
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COTTP26
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Q9NFJ8;
Q1-OCT-2000 (TEMBLrel. 15, C)
01-OCT-2000 (TEMBLrel. 15, L6
01-OCT-2002 (TEMBLrel. 22, L6
Histone H1.
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                             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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Result No.

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4; Gaps

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                                                                                                                                                                                                                                                                                                                        Name=H1B76;
Trypanosoma brucei gambiense.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=31285;
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Grueter E.;
Thesis (2000), Department of Parasitology, Institute of Zoology,
SWITYERLAND.
                                                                                                                                                                                                                                                                                                                                                                                                         Grueter E.;
Thesis (2000), Department of Parasitology, Institute of Zoology,
SWITZERLAND.
                                                                                                             Score 102.5; DB 2; Length 71; Pred. No. 1; 4; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.9%; Score 102; DB 2; Length 76; 48.1%; Pred. No. 1.2; tive 4; Mismatches 27; Indels
                                    SEQUENCE FROM N.A.
STRAIN=STIB 755;
Grueter E., Betschart B.;
Submitted (ABL/GenBank/DDBJ databases.
EMBL, AJ287594; CAB76176.1; -.
SEQUENCE 71 AA; 7019 MW; 6C7DED4F3B75D8C4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=STIB 755, and 1257;
GTUELER E., Beteschart B.;
Submitted (FEB-2000) to the
EMBL; AJ287595; CAB76177.1; -.
EMBL; AJ272462; CAB76172.1; -.
SEQUENCE 76 AA; 7516 MW; 48882064F7B9A6F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
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01-0CT-2000 (TEMBLrel. 15, Last seq
05-JUL-2004 (TEMBLrel. 27, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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01-OCT-2000 (TrEMBLrel. 15, C;
01-OCT-2000 (TrEMBLrel. 15, L;
01-OCT-2002 (TrEMBLrel. 22, L;
Histone H1.
Name=H1G76;
                                                                                                              28.0%;
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                                                                                                                                                                                                73
                                                                                                                                                                                                                  58 PKKVAGKKAAKKA 71
                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=STIB 755, and 1257;
                                                                                                        20.0.
Best Local Similarity 50.00
Matches 37; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AKKYAKKEKAYAKKA--EKAA-KKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAA
Trypanosoma brucei brucei.
Eukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae, Trypanosoma.
NCBI_TaxID=5702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBL_TaxID=5702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                    SEQUENCE FROM N.A.
STRANI+427;
Grueter E.;
Thesis (2000), Department of Parasitology, Institute of Zoology,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Grueter E.;
Thesis (2000), Department of Parasitology, Institute of Zoology,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.9%; Score 102; DB 2; Length 76;
49.4%; Pred. No. 1.2;
tive 2; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25; Indels
                                                                                                                                                                                                                                                                                                                                  Grueter E., Betschart B.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ204607; CAB76192.1; -
SEQUENCE 76 AA; 7505 MM; 83BES0D89F1BEDBF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SECUENCE FROM N.A.
STRAIR=TREU 92774;
Grueter E., Betechart B.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ400880; CAB90837.1; -.
EMBL; AJ287606; CAB76191.1; -.
EMBL; AJ287605; CAB76197.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=TREU 927/4;
Grueter E., Betschart B.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 AA; 7019 MW; 406BE51794847C80 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2004 (TrEMBLrel. 27, Last annotation update)
Histone H1.
Name=H1D71; Synonyms=H1B71, H1C71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 AEAKYKAEAAKAAAKEA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 KPLAKKVAGKKAAKKA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 49.4
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38; Conservative
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us-10-792-311-5.rup

Q9NFF2 Q9NFF2;

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2 AKASAAPKKAVAKKAAPKKAVAKKAAPKKAVAKKAAPKKAVAKKAAPKKVAPK 59
2 AKASAAPKKAVAKKAAPKKAAPKKAVAK--KAAPKKAVAKKAAPKKAVAKKPLAKKVVAK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AKKYAKKEKAYAKKA--EKAA-KKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trypanosoma brucei brucei.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5702;
                                                                                                                                                                                                                                                                     Name=H1E71; Synonyms=H1A71;
Trypanosoma brucei brucei.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5702;
                                                                                                                                                                                                                                                                                                                                                                                                          Grueter B.;
Thesis (2000), Department of Parasitology, Institute of Zoology,
SWITZERLAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=TREU 927/4;
Grueter E.;
Theeis (2000), Department of Parasitology, Institute of Zoology,
SWITZERLAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26.4%; Score 96.5; DB 2; Length 71; 48.7%; Pred. No. 2.8; tive 4; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=TREU 927/4;
Grueter E., Betschart B.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ400881; CAB90839-1; -.
EMBL; AJ207600; CAB76185-1; -.
SEQUENCE 71 AA; 7005 MW; 478C7B6994847C80 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=TREU 927/4;
Grueter E., Betschart B.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last seq
05-JUL-2004 (TrEMBLrel. 27, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Histone H1.
Name=H1D76; Synonyms=H1A76, H1C76;
                                                                                                                                                                               PRT;
                                                     73
                                                                                    60 KVAPKKVAGKKAAKKA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | |||||:|
60 ----KVAGKKAAAKKA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 EAKYKAEAAKAAAKEA 73
                                                      57 AEAKYKAEAAKAAAKEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37; Conservative
                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 37; Conserv
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN=TREU 927/4;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                   Histone H1.
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                                                                                                                                                                                               Q9N6K0
                                                                                                                                                                             Q9N6K0
                                                                                                                                            RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AKKYAKKEKAYAKKA--EKAA-KKAEAKAYKAAEAKKKAKAEAKKYAKAAK-AEKKEYAA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 AKTTAAPKKAVAKKAAPKKAAPKKAVAK--KAAPKKAVAKKAAPKKAVAKKPLAKKVVAK 59
                                                                                                                                                                                              Trypanosoma brucei brucei.
Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Histone H1.

Name-H1B76;

Trypanosoma brucei brucei.

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.

NCBI_TaxID=5702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Grueter E.;
Thesis (2000), Department of Parasitology, Institute of Zoology,
                                                                                                                                                                                                                                                                                                                    Grueter E.;
Thesis (2000), Department of Parasitology, Institute of Zoology,
SWITZERLAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 99; DB 2; Length 76;
Pred. No. 1.9;
3; Mismatches 29; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 99; DB 2; Length 76;
Pred. No. 1.9;
3; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=TREU 927/4;
Grueter E., Betschart B.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ400880; CAB90836.1; -.
SEQUENCE 76 AA; 7631 MW; 2493E88448B3E0FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=TREU 927/4;
Grueter B., Betschart B.;
Submitted (FEB-JOB) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ287599; CAB76182.1; -.
SEQUENCE 76 AA; 7587 MW; 2959EF4982B2E0F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                         76 AA.
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                                                                                                                            Created)
                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57 AEAKYKAEAAKAAKEA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | | | | |||||:|
KVAPKKVAGKKAAAKKA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.0%;
50.6%;
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50.6%;
     ----KVAGKKAAAKKA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 50.64
Matches 39, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 50.69
Matches 39, Conservative
                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                    STRAIN-TREU 927/4;
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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Q9NPJ6; Q9NFJ6

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RESULT 7 29NFJ6

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2 AKASAAPKKAVAKKAAPKKAAPK-KGAPKKAVAK--KGAPKKAVAKKAAPKKAVAKKPLAKKVVAK 59
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                                                                                                                                                                                                                                             Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5702;
                                                                                                                                                                                                                                                                                                                                                                                                 Grueter E.;
Thesis (2000), Department of Parasitology, Institute of Zoology,
SWITZERLAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 26.0%; Score 95; DB 2; Length 76; Best Local Similarity 49.4%; Pred. No. 3.8; Matches 38; Conservative 3; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=TREU 927/4;
Grueter E., Betschart B.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ287601; CAB76190.1; -.
EMBL; AJ287601; CAB76186.1; -.
SEQUENCE 76 AA; 7573 MW; 6079EF4982B50767 CRC64;
                                                                                01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Histone H1.
                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 KVAPKKVAGKKAAKKA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=H1A75;
Trypanosoma brucei gambiense.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 25.3%;
Best Local Similarity 51.4%;
Matches 37; Conservative
                                                                                                                                                                                                           Synonyms=H1F76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 AEAKYKAEAAKAAKEA
                                                                                                                                                                                                                                       Irypanosoma brucei brucei
                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=TREU 927/4;
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01-OCT-2000
01-OCT-2002
                                                                                                                                                                                                              Name=H1E76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Histone H1.
                                                       Q9N6IO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O9NFK0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9NFK0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AKKYAKKEKAYAKKA--EKAA-KKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 AKASAAPKKAVAKKAAPKKAVAK -- KAAPKKAVAKKAAPKKAVAKKPLAKKAAPK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AKKYAKKEKAYAKKA--EKAA-KKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 AKTTAAPKKAVAKKAAPKKAAPKKAVAK--KAAPKKAVAKKAAPKKAVAKKPLAKKAAPK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Grueter E.;
Thesis (2000), Department of Parasitology, Institute of Zoology,
SWITZERLAND.
                                                                                                                                                                                                                                                                                                                                                                                                             ch 26.2%; Score 96; DB 2; Length 76; Il Similarity 49.4%; Pred. No. 3.2; 38; Conservative 5; Mismatches 28; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 96; DB 2; Length 76;
Pred. No. 3.2;
5; Mismatches 28; Indels
                     Grueter E., Betschart B.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ287600; CAB76181.;
EMBL, AJ287599; CAB76183.1;
EMBL, AJ287598; CAB76181.1;
CGC, GO:000786; C:nucleosome; IEA.
GO; GO:000534; C:nucleosi IEA.
GO; GO:000534; P:DNA binding; IEA.
GO; GO:000534; P:DNA binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-TREU 927/4;
Grueter E., Betschart B.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ4008H1, CAB90838.1; -.
GO; GO:0000786; C:nucleosome; IEA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005634; P:DNA binding; IEA.
GO; GO:000334; P:DNLCLeosome assembly; IEA.
                                                                                                                                                                                                                                                                                                                       PRINTS; PRO0624; HISTONEHS. _
SEQUENCE 76 AA; 7556 MW; 2959F33D5D55B0F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7601 MW; 2493F4F09754B0FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                              IPR005819; Histone_H5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR005819; Histone H5. PRINTS; PR00624; HISTONEH5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : | | | | |||||:|
60 KVAPKKVAGKKAAAKKA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 E-AKYKAEAAKAAAKEA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 KVAPKKVAGKKAAAKKA 76
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Best Local Similarity 49.4%;
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Irypanosoma brucei brucei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=TREU 927/4;
STRAIN=TREU 927/4;
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                                                                                                                                                                                                                                                                                                 InterPro;
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RESULT 10

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Gaps

9

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13 KKVAAK-KAVAKKA-APKKAVAK--KAAPKKAVAKKAAPKKAVA----KKVVAKKVAPK 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 KKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAKY 61
                                                                                                                                                             Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBL_TaxID=31285;
                                                                                                                                                                                                                                                                                                                    Grueter E.;
Thesis (2000), Department of Parasitology, Institute of Zoology,
SWITZERLAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
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Pred. No. 5.6;
1; Mismatches 25; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=STIB 755;
Grueter E., Betschart B.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ28792; CAB06174.1; -.
SEQUENCE 75 AA; 7597 MW; 130AB85471996052 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130AB85471996052 CRC64;
(TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 22, Last annotation update)
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RESULT 11

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12;

H1C8_TRYCR

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1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKA--KAEAKKYAKAAKAEKKEYAAAE 58
                                                                                                                                                                                                                                                2 AKASAAPKKAVAKKA--APKKA--APKKAVAKKAAPKKAVAKK----PLAKKVVAKKV 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                               Score 86; DB 2; Length 66;
Pred. No. 15;
2; Mismatches 25; Indels
                                                        EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jedrusik M.A., Schulze E.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WormBase Consortium;
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cosmid C01B10.";
EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=Bristol N2;
STRAIN=Erriston ST
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to the EMBL/GenBank/DDBJ databases
                                                                                      2D664C3471064DC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Histone H1.Q (Histone h1 like protein 7, isoform c)
                                                                                                                                                                                                                                                                                                                                                                                                                             60 AA
                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=hil-7; ORFNames=C01B10.5;
Caenorhabditis elegans.
                                  Grueter E., Betschart B.;
Submitted (FEB-2000) to the
EMBL; AJ287608; CAB76193.1;
SEQUENCE 66 AA; 6593 MW;
                                                                                                                                 ch 23.5%;
l Similarity 48.0%;
36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Bristol N2;
Blanchard M., Bradshaw H.;
"The sequence of C. elegans
Submitted (MAY-1996) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF216291; AAF23175.1;
EMBL; US8757; AAK66021.1; -.
                                                                                                                                                                                                                                                                                        59 AKYKAEAAKAAKEA 73
                                                                                                                                                                                                                                                                                                                              52 APKKVAGKKAAAKKA 66
                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wilson R.;
Submitted (DEC-2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wilson R.;
Submitted (JUL-2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NormBase Consortium;
                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-Bristol N2;
SEQUENCE FROM N.A. STRAIN=427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9U3W3;
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                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67
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                                                                                                                                                                                                                                        Trypanosoma cruzi.
Bukaryota: Buglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L27116; AAA66480.1; -.
EMBL; L27118; AAA66482.1; -.
INCEPTO; IPRO05819; Histone H5.
PRINTS; PR00624; H1STONEH5.
Chromosomal protein; DNA-binding; Multigene family; Nuclear protein.
SEQUENCE 74 AA; 7688 MW; 036AF6C72BB0249B CRC64;
                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95059220; PubMed=7969272; DOI=10.1016/0166-6851(94)90082-5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Grueter B.;
Thesis (2000), Department of Parasitology, Institute of Zoology,
SWITZERLAND.
[2]
                                                                                                                                                                                                                                                                                                                                                                                       Aaslund L., Carlsson L., Henriksson J., Rydaaker M., Toro G.C., Galanti N., Pettersson U.;
"A gene family encoding heterogeneous histone H1 proteins in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.0%; Score 88; DB 1; Length 74; 47.1%; Pred. No. 12; 26; Indels tive 3; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                 HIC8_TRYCR STANDARD; PRT; 74 AA. P40270; P40272; 01-P81-1995 (Rel. 31, Created) U-NOV-1995 (Rel. 32, Last sequence update) 01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trypanosoma cruzi.";
Mol. Biochem. Parasitol. 65:317-330(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Frypanosoma brucei brucei.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 47.1 tes 33; Conservative
73
                                    64 KVAGKKAAAKKA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 AAAKEAAYEA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 KAPKKAVKKA 70
KAEAAKAAAKEA
                                                                                                                                                                                                                                Histone H1.C8/H1.M1.
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=Tulahuen 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Histone Hl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O9NFJ3;
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Q9NFJ3

RESULT 14

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0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

23.2%; Score 85; DB 2; Length 60;
Best Local Similarity 43.4%; Pred. No. 16;
Matches 23; Conservative 4; Mismatches 26; Indels
WormBase; WBGene00001858; hil-7.
WormPep; C01B10.5c; CE26857.
G0; G0:0000786; c:nucleosone; IEA.
G0; G0:0005634; C:nucleus; IEA.
G0; G0:000534; P:nucleosone assembly; IEA.
G0; G0:00063134; P:nucleosone assembly; IEA.
FILLETPRO; IPRO05819; Histone—H5.
FRINTS; PRO0584; HISTONERS.
SEQUENCE 60 AA; 6212 MW; D01ABB4CEC35566D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: June 3, 2005, 11:15:30 Job time: 173 secs
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OM protein - protein search, using sw model

June Run on:

3, 2005, 10:57:41 ; Search time 157 Seconds (without alignments) 189.685 Million cell updates/sec

US-10-792-311-5 366 ritle:

Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1079814 Total number of hits satisfying chosen parameters:

2105692 seqs, 386760381 residues

Searched:

DB seq length: 0 DB seq length: 77 Minimum I Maximum I Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_16Dec04:* geneseqp1980s:* Database

geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2002s:*

geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Description	Aay82575 Copolymer	_	Aay82573 Copolymer	_	_	-	Aaw24449 Nucleic a	Ado43176 Peptide u	Ado04487 Sea urchi	Ads15345 Yeast zuo	Aar28871 High affi	Adel0646 Structura	Adk15665 Nucleatin	Aam17388 Peptide #	Abb36406 Peptide #	Abb21763 Protein #	Aam69569 Human bon	Abg39191 Human pep	Aaw08392 Nucleic a	Aaw38225 Peptide u		Aaw52872 Nucleic a	Adel0603 Structura	Adk15622 Nucleatin	Ado04488 Chicken h
ΩI	8	AAY82574	AAY82573	AAY82572	AAY82571	ABG71043	AAW24449	ADO43176	AD004487	ADS15345	AAR28871	ADE10646	ADK15665	AAM17388	ABB36406	ABB21763	AAM69569	ABG39191	AAW08392	AAW38225	AAW69201	AAW52872	ADE10603	ADK15622	ADO04488
DB	m	m	ო	m	ო	ហ	~	œ	80	œ	7	7	œ	4	4	4	4	ഗ	7	~	<b>~</b>	~	7	œ	æ
% Query Match Length	77	99	26	45	35	9	46	26	9	9	46	75	75	71	71	71	71	71	61	61	61	61	70	70	61
% Query Match	100.0	77.2	67.1	35.8	28.6	28.3	27.7	27.7	27.7	27.7	27.2	26.8	26.8	25.4	25.4	25.4	25.4	25.4	25.1	25.1	25.1	25.1	24.6	24.6	24.3
Score	366	282.5	245.5	131	104.5	103.5	101.5	101.5	101.5	101.5	99.5	86	86	93	93	93	93	93	92	92	92	92	90	90	89
Result No.		7	m	4	S	9	7	80	0	10	11	12	13	14	. 15	16	17	18	19	20	21	22	23	24	25

•	Adel0647 Structura	Adk15666 Nucleatin	Adr96126 Novel S.	Aao05530 Human pol	Adel0696 Structura	Adk15715 Library f	Aael3239 Human lin	Ado43172 Peptide u	Adel0653 Structura	Adk15672 Library f	Aay98495 Nuclear l	Aay59040 Nuclear 1	Aab45848 Nucleic a	Aau04285 Nuclear l	Aae13238 Human lin	Aar90180 Polycatio	Aaw06686 Protamine	Aar90181 Polycatio	Aaw06688 Protamine
ADS15346	ADE10647	ADK15666	ADR96126	AA005530	ADE10696	ADK15715	AAE13239	AD043172	ADE10653	ADK15672	AAY98495	AAY59040	AAB45848	AAU04285	AAE13238	AAR90180	AAW06686	AAR90181	AAW06688
œ	7	æ	æ	4	7	œ	ß	æ	7	80	m	٣	4	4	'n	N	~	~	7
61	67	67	69	75	75	75	99	49	70	70	59	29	59	59	77	32	32	33	33
24.3	24.3	24.3	24.3	24.3	24.3	24.3	24.2	24.0	23.8	23.8	23.5	23.5	23.5	23.5	23.5	23.1	23.1	23.1	23.1
83	83	89	89	89	89	89	88.5	88	87	87	98	98	98	98	82	84.5	84.5	84.5	84.5
56	27	28	59	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

AAY82575 standard; peptide; 77 AA. RESULT 1

28-JUL-2000 (first entry) AAY82575; 

Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:5.

Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic: immunosuppressive; demyalinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.

Unidentified

WO200018794-A1.

06-APR-2000.

99WO-US022402. 24-SEP-1999; 98US-0101693P. 25-SEP-1998; (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.

Gad A, Lis D;

WPI; 2000-317499/27.

Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.

Claim 10; Page 14; 72pp; English.

AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention of scribes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides

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acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either inediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating arthritis, such diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune thrombocytopaenia purpura, colitis, contact sensitivity disease, thrombocytopaenia purpura, colitis, contact sensitivity disease, disease, idiopathic myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated mediated diseases which can be treated include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKKAKAEAKKYAKAKAKAEKKEYAAAAEAK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                glatiramer acetate; autoimmune disease; antiathritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; osteopathic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.
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                                                                                                                                                                                                                                                                                                          properties which are analogous to glatiramer acetate molecules, which
makes them ideal for use as molecular weight markers
                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:4.
of the invention are used as molecular weight markers for glatiramer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Copolymer; molecular weight marker; TV-marker; immune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 366; DB 3; Length 77;
; Pred. No. 7.7e-27;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY82574 standard; peptide; 66 AA.
                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 YKAEAAKAAAKEAAYEA 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-US022402
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                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity luv..
77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-JUL-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-317499/27.
                                                                                                                                                                                                                                                                                                                                                                      Sequence 77 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200018794-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lis D;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY82574;
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Way 82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glattramer actate invention are used as molecular weight markers for glattramer actate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases of treating and preventing immune diseases in a mammal. Autoimmune diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid archititis, osteoarchritis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune thyroiditis, autoimmune thyroiditis, autoimmune thyroiditis, autoimmune viceocephic conditions, disease, chronic immune thyroiditis, autoimmune thyroiditis, autoimmune spronic particular sensitivity disease, diabetes mellitus, Graves disease, dialated conditions, demy purpura, colitis, conteat sensitivity disease, diabetes mellitus, Graves disease, dialated conditions wilgaris, or systemic lupus erythematosus. Mediated conditions wild delayed-type hypersensitivity. The mediated diseases and delayed-type hypersensitivity. The properties which are analogous to glativamer actate molecules, which
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    syndrome; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyromimetic; harmostatic; antipsoriatic; dermaclogical; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diabetes mellitus; Graves disease; Guillain-Barre's syndrome;
Hashimoto's disease; idiopathic myxoedema; myasthenia gravis;
pemphigus vulgaris; systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77.2%; Score 282.5; DB 3; Length 66; 84.4%; Pred. No. 3.6e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      properties which are analogous to glatiramer acetate makes them ideal for use as molecular weight markers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY82573 standard; peptide; 56 AA.
                        Claim 10; Page 14; 72pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-JUL-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diabetes mellitus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 66 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200018794-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unidentified
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(YEDA ) YEDA RES & DEV CO LTD.

Weight TV-marker polypeptides from the present invention. The present weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated iseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune thrombocytopaenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Grohn's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, postiated diseases which can be treated include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical process. Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases. properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as molecular weight markers Claim 10; Page 14; 72pp; English. (TEVA-) TEVA PHARM USA INC WPI; 2000-317499/27 Gad A, 

Sequence 56 AA;

1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAKAEAKKYAKAKAKEKKEYAAAEAK 60 1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKK--------AEAK 39 0; Indels 21; Gaps 67.1%; Score 245.5; DB 3; Length 56; 72.7%; Pred. No. 8.1e-16; Live 0; Mismatches 0; Indels 21 Query Match
Best Local Similarity 72.7
Matches 56; Conservative

61 YKAEAAKAAKEAAYEA 77 YKAEAAKAAAKEAAYEA 56

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AAY82572 standard; peptide; 45 AA.

28-JUL-2000 (first entry) AAY82572;

Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:2.

optormer, margine many transfer and architich memora optormer; margine many optormer; margine many optormer; memora obteopathic; memunosuppressive; antithyroid; antiphoriatic; dermatory; antidabetic; thyromimetic; haemostatic; antiphoriatic; dermatory; antiphoriatic; dermatory condition; multiple sclerosis; rheumatoid arthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; permit pemphigus vulgaris; systemic lupus erythematosus. Copolymer; molecular weight marker; TV-marker; immune disease; 

WO200018794-A1.

06-APR-2000

99WO-US022402 24-SEP-1999;

98US-0101693P. 25-SEP-1998; YEDA RES & DEV CO LTD. TEVA PHARM USA INC. (YEDA ) YEDA TEVA-)

Gad A, Lis D;

MPI; 2000-317499/27.

Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases

Claim 10; Page 14; 72pp; English

MAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include either cell-mediated or antibody-mediated diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune hemolytic anaemia, autoimmune cophoritis, autoimmune thyroididis, e.g. multiple sclerosis, contact arthritis, outoimmune thyroididitis, autoimmune uveoretinitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic mysacedema, myasthenia gravis, perminance, mediated disease, undelayed-type hypersensitivity. The mediated disease, and delayed-type hypersensitivity. The properties which are analogous to glatiramer acetate molecules, which are analogous to glatiramer acetate molecules, which 

Sequence 45 AA;

32; 35.8%; Score 131; DB 3; Length 45; 50.6%; Pred. No. 2.6e-05; ive 0; Mismatches 6; Indels Local Similarity 50.6 nes 39; Conservative Query Match Matches

3

1 AKKYAKKEKAYAKKAEKAAKKAEAAKAYKAAEAKKKAKAEAKKYAKAAAKAEKKEYAAAEAK 60 1 AKKYAKK----AKAEKA----KKAYKAAEAKKAAKYE---

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AAY82571 ID AAY RESULT

AAY82571 standard; peptide; 35 AA. 

(first entry)

28-JUL-2000

Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:1.

Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antidianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis;

Unidentified

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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer coff the invention are used as molecular weight markers for glatiramer treated tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune thrombocytopaenia purpura, collitis, contact sensitivity disease, diabetes mellitus, Garves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, sporiasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated mediated diseases which can be treated include host-versus-graft disease, and delayed-type hypersenaitivity. The golypeptides of the invention have defined molecular weights and physical
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                     diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis;
Hashimoto's disease; idiopathic myxoedema; myasthenia gravis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                properties which are analogous to glatiramer acetate molecules, which
makes them ideal for use as molecular weight markers
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Crohn's disease; chronic immune thrombocytopaenia purpura; colitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumour neoangiogenesis associated peptidase substrate peptide #7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3; Length 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 104.5; DB 3; Length
Pred. No. 0.0058;
4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40 AKKYAKAAKAEKKEYAAAEAKYKAEAAKAAAKEAAYEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 10; Page 14; 72pp; English.
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                                                                                                                                                                                                                                                                                                       (YEDA ) YEDA RES & DEV CO LTD (TEVA-) TEVA PHARM USA INC.
                                                                                                                                                                                                                           99WO-US022402
                                                                                                                                                                                                                                                                   98US-0101693P
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Best Local Similarity 65.8°
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          VPI; 2000-317499/27
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                                                                                                                                         WO200018794-A1
                                                                                                                                                                                                                                                                                                                                                                      Lis D;
                                                                                                   Unidentified
                                                                                                                                                                                                                           24-SEP-1999;
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tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inducing molecules. The molecules are useful as a medicine and in the manufacture of a medicament for the treatment and/or prevention of tumo related disorders. The compounds are able to induce blood clotting at tumour sites resulting in the disruption of the tumour vascularisation and consequently in the control of tumour growth. This sequence represents a heparin-binding peptide, a postively charged polymer that can be incorporated into a substrate for extracellular hydrolases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New tumor-selective intravascular coagulation inducing molecules useful
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blood clotting; tumour vascularisation; tumour growth control;
heparin-binding peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       releasable by tumour or neoangiogenic endothelial cells
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Pred. No. 0.013;
5; Mismatches 19;
                                                                                             /note= "Optionally absent"
19. .24
/note= "Optionally absent"
                                                                         . .12
note= "Optionally absent"
                                                                                                                                             ...42
ote= "Optionally absent"
                                                                                                                                                                                                                   .48
te= "Optionally absent"
                                                                                                                                                                                                                                                                   Misc-difference 55. .60 /note= "Optionally absent"
                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28.3%;
                                                                                                                                                                                                                                                                                                                                                       30-JAN-2002; 2002WO-EP000951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for control of tumor growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34; Conservative
                                                                                                                                                                                                                                   /note=
                                                                                                                                                                                                           /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 YKAEAAKAA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50 KKARAAKKA 58
                                                                                                                                                                                                                                                                                                                                                                                                                               Trouet A, Dubois V;
                                                                                                Misc-difference 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-706887/76.
                                                                                                                                                                                                                      Misc-difference 43.
                                                                                                                        Misc-difference 19
                                                                                                                                                                                                                                             Misc-difference 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                              Misc-difference 37
                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 60 AA;
                                                                                                                                                                                                                                                                                                         WO200260488-A1
                                                                                                                                                                                                                                                                                                                                 08-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 7
AAW24449
ID AAW2
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The present sequence is that of a peptide of potential use for production of a coded probe useful in the method of the invention. The invention provides methods, apparatus and compositions for the detection. The detection, identification and/or sequencing of biomolecules, such as nucleic acids or proteins. Coded probes comprising a probe molecule strached to one or more nano-barcodes are allowed to bind to target molecule (8). After binding and separation from unbound coded probes, the bound coded probes are aligned on a surface and analysed by scanning probe microscopy (SPM). The methods allow the sequencing of long nucleic acid sequences in a single sequencing run, high speed of obtaining sequence data, low cost of sequencing and high efficiency in terms of operator time, and sensitive and accurate detection and/or identification of nucleic acids with low incidence of false positive results.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Macroscopic membrane; cell growth, EAK16; Z-DNA binding protein; zuotin; addical product; suture; artificial skin; internal lining; slow-diffusion drug delivery system; protein-type drug; erythropoietin; haemoglobin; insulin; cell adhesion; cell migration; Alzheimer's disease;
                                                                                                                                                                                          Detecting, identifying and sequencing of biomolecules using controlled alignment of nano-barcodes encoding specific information for scanning probe microscopy, useful in the fields of molecular biology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 AEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKAAAKEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 далаақлалалалалалалалалалалалалалан 2. далалалалалалалала
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 27.7%; Score 101.5; DB 8; Length 56; Local Similarity 55.9%; Pred. No. 0.018; es 33; Conservative 0; Mismatches 21; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                scrapie infection; sea urchin; histone; H1; variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sea urchin histone H1 variant protein.
                                                                                                                                                                                                                                                                                 Example 2; Page 44; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADO04487 standard; protein; 60 AA
20-SEP-2002; 2002US-00251152.
19-SEP-2003; 2003US-00667004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92US-00973326.
94US-00293284.
97US-00824515.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-MAR-2003; 2003US-00390472
                                                                                                           Yamakawa M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RICH A.
DIPERSIO C M.
LOCKSHIN C.
                                                                                                                                               WPI; 2004-399960/37.
                                                               (ITLC ) INTEL CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arbacia punctulata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HOLMES T.
ZHANG S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US2004087013-A1.
                                                                                                           Su X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 56 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-AUG-1994;
26-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-MAY-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADO04487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HOLM/)
(ZHAN/)
(RICH/)
(DIPE/)
                                                                                                           Chan S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (LOCK/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AD004487
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      condensing and stabilising a NA. The peptides can be conjugated to a lytic peptide to form a nucleic acid transporter system. The lysis agent forms an alpha-helical structure. The transporter system is used to deliver nucleic acid to a cell and for treating humans by gene therapy. By taking advantage of the characteristics of both the lysis agents and the binding molecules, delivery of the nucleic acid is enhanced. Specific lysis agents are capable of releasing the nucleic acid into the cellular interior from the endosome. Release is efficient without
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             endosomal/lysosomal degradation. Once released the binding complexes help target the nucleic acid to the nucleus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW24434-W24459 are nucleic acid (NA) binding peptides, capable of both
                                                                                                                           Nucleic acid transporter; gene therapy; binding complex; lysis agent; JTS-1; KB; alpha helix; endosome; lysosome; nucleus targeting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid transporter useful in gene therapy - contains binding complex associated with surface and nuclear ligands and lysis agent
                                                                               Nucleic acid (NA) binding peptide used in NA delivery to cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.7%; Score 101.5; DB 2; Length 46; 58.7%; Pred. No. 0.015; tive 6; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 KAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAKYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nano-barcode; scanning probe microscopy; probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide used for coded probe synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 49; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                 (BAYU ) BAYLOR COLLEGE MEDICINE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADO43176 standard; peptide; 56
                                                                                                                                                                                                                                                                                                                            96WO-US005679.
                                                                                                                                                                                                                                                                                                                                                                        95US-00484777.
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                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sparrow JT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-052345/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      402004038037-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 46 AA;
                                                                                                                                                                                                                                                                                                                                                                     07-JUN-1995;
                                                                                                                                                                                                                                                                                                                          23-APR-1996;
                                         30-SEP-1997
                                                                                                                                                                                                                                        409640958-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JUL-2004
                                                                                                                                                                                                                                                                                 19-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-MAY-2004
                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADO43176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smith LC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Best Loc Matches

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RESULT 8 ADO43176

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5; Gaps

73

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involves adding a macroscopic membrane that is formed by self-assembly of amphibhilic peptide in an aqueous solution containing monovalent metal cations to a cell culture medium comprising cells, thus forming a membrane/culture mixture, maintaining the mixture under conditions cufficient for cell growth. The invention also relates to EAX16 peptide derived from yeast 2-DNA binding protein (zuotin). Zuotin incorporated into the macroscopic membranes are useful in biomaterial applications such as medical products (e.g., sutures), artificial skin or internal linings, slow-diffusion drug delivery systems supports for in vitro cell growth or culture and support for artificial tissue for in vitro cell conductive biopolymer for culturing cell worldiffusion drug delivery vehicle for delivering protein-type drugs conductive biopolymer for culturing cell monolayers, for promoting cell adhesion and migration, useful as experimental models for Alzheimer's disease and scrapic infection. The present sequence is sea urchin histone HI variant protein. This sequence is used to illustrate the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
H
                                                                                             Novel EAK16 protein incorporated into macroscopic membranes, useful in
biomaterial applications such as medical products, artificial skin or
internal linings, slow-diffusion drug delivery systems for in vitro cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 KKYAKKEKAYAKKAEKAAK-KAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KAAAKRKAALAKKKAAAAKRKAAKKAKKPKKKAAKKAAKKPAKKSPKKAKKPAKKSPK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cell culture; macroscopic membrane; amphiphilic peptide; biomaterial; jour-diffusion drug delivery system; artificial skin; separation matrix; Alzheimer's disease; scraple; liver cirrhosis; kidney amyloidosis; protein conformational disease; yeast; DNA binding protein; zuotin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Gaps
                                                                                                                                                                                                                                        invention relates to a method for in vitro cell culture which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27.7%; Score 101.5; DB 8; Length 60; 48.3%; Pred. No. 0.02; ive 7; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lockshin C;
                    Dipersio CM, Lockshin C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rich A, Dipersio CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yeast zuotin homologue sea urchin H1 delta.
                                                                                                                                                                                               Example 5; SEQ ID NO 16; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MASI ) MASSACHUSETTS INST TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADS15345 standard; protein; 60 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97US-00824513.
                  Rich A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92US-00973326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94US-00293284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 Similarity 48.3%;
29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-DEC-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Paracentrotus lividus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sea urchin; H1 delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Holmes T, Zhang S,
                    Zhang S,
                                                          WPI; 2004-356208/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 60 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US6800481-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-OCT-2004
                                                                                                                      biomaterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nvention.
                  Holmes T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADS15345;
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ADS15345
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The invention describes a method of culturing (M1) cells, in vitro. The cell culture involves adding a macroscopic membrane which is formed by self-assembly of amphiphilic peptides in an aqueous solution containing monovalent metal cations, where the peptides have alternating hydrophobic and hydrophilic amino acids and are complementary and structurally compatible, to a cell culture medium comprising cells, thus forming a membrane/culture mixture, and maintaining the mixture under conditions sufficient for cell growth. (M1) is useful for culturing a macroscopic membrane utilised in biomaterial applications e.g., slow-diffusion drug cellivery systems, artificial skin or separation matrices, or as experimental models for Alzheimer's disease and scrapic infection e.g., liver cirrhosis, kidney amyloidosis, or other protein conformational diseases. (M1) enables in vitro culturing of macroscopic membrane that is stable in aqueous solution, serum and ethanol, highly resistant to heat, alkaline and acidic ph, chemical denaturants and proteolytic digestion, and is non-cytotoxic. This is the amino acid sequence of a region found in sea urchin histone H1 delta which is homologous to yeast DNA binding protein zuctin from which amphiphilic peptides capable of forming
                                    Culturing cells, in vitro, by adding macroscopic membrane formed by self-assembly of amphiphilic peptides and monovalent metal cations, to form culture mixture, and maintaining culture mixture under conditions for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                glycopeptide, mannose; mannosylated, glycosylated; mannose receptor; macrophages; monocytes; destroy; cytotoxicity; label; image; alter; macrophage processing of antigen; MRC restriction; inflammation; inflammatory diseases; macrophage secretory products; Crohn's disease; legionnaires disease; mononuclear phagocytes; HIV; AIDS; lysosomal storage diseases; Gaucher's disease; asthma; alveolar macrophages metastasis; systemic macrophages; deliver; antigenic peptides; prevent transplant rejection; organ transplantation; antitumour agents; cancer; toxins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "opt may have mannose, fucose, glucose or N-Ac-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 KKYAKKEKAYAKKAEKAAK-KAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "opt may have mannose, fucose, glucose or N-Acglucosamine. May also have non interfering substits."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "opt may have mannose, fucose, glucose or N-Ac-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High affinity macrophage mannose receptor ligand compound #9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27.7%; Score 101.5; DB 8; Length 60; 48.3%; Pred. No. 0.02; tive 7; Mismatches 23; Indels 1
                                                                                                                                                  Example 5; SEQ ID NO 16; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR28871 standard; peptide; 46 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       glucosamine."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glucosamine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 48.3
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  membrane can be isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
WPI; 2004-707224/69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 60 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                           cell growth.
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23-MAR-1993
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controlling metastasis, mediated by systemic macrophages. The peptides can also be used to deliver antigenic peptides as conjugates to a macrophage to macrophage to macrophage to macrophage to macrophage. Also self peptides to prevent tissue transplant rejection. (Updated on 25-MAR-2003 to correct P

3,

Gaps

11;

Score 99.5; DB 2; Length 46; Pred. No. 0.023; 3; Mismatches 9; Indels 1

27.2%;

Sequence 46 AA;

field.)

33; Conservative

ADE10646 standard; protein; 75 AA.

14 KAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKAA 69

10 /note= "opt may have mannose, fucose, glucose or N-Ac- glucosamine."	/note= "opt may have mannose, fucose, glucose or N-Acglucosamine."	/note= "opt may have mannose, fucose, glucose or N-Ac-glucosamine."	<pre>//note= "opt may have mannose, fucose, glucose or N-Ac- glucosamine."</pre>	/note= "opt may have mannose, fucose, glucose or N-Ac-glucosamine."	/note= "opt may have mannose, fucose, glucose or N-Ac-glucosamine."	/note= "opt may have mannose, fucose, glucose or N-Ac-glucosamine."	/note= "opt may have mannose, fucose, glucose or N-Ac-glucosamine."	/note= "opt may have mannose, fucose, glucose or N-Ac-glucosamine."	/note= "opt may have mannose, fucose, glucose or N-Ac-glucosamine."	/note= "opt may have mannose, fucose, glucose or N-Ac- glucosamine."	/lote= "opt may have mannose, fucose, glucose or N-Ac-	40. /note= "opt may have mannose, fucose, glucose or N-Ac- glucosamine. May also have non interfering substits."			92WO-US003609.	91US-00694983.	WASHINGTON.		316/48.	affinity mannose receptor ligand cpds for treating diseases by macrophage activity e.g. asthma, inflammatory diseases and is diseases, e.g. HIV.	21; 32pp; English.	This compound represents a glycopeptide effective in inhibiting the binding of labelled mannosylated BSA to mannose receptors. Mannose receptors are uniquely found on macrophages and not on monocytes. Glycopeptides such as this provide a mechanism to target macrophages specifically, to image, label, destroy or otherwise alter their antigen specifically, to image, label, destroy or otherwise alter their antigen processing function. In addition they can be conjugated to solid supports and used to purify mannose receptors from a variety of sources. They are useful in the treatment of inflammatory diseases driven by macrophage serretory products eg. Crohn's disease; infectious diseases in which macrophages harbour replicating infectious agents eg. Legionnaires disease; viral infections involving mononuclear phagocytes eg. HIV and lysosomal storage diseases, in which macrophages are principally involved eg. Gaucher's disease; and in in
Modified-site	Modified-site	Modified-site	Modified-mite	W	מקיים ביים ביים	אַטקיָנָיָם בְּיִבְּיִם אָיִנְיָם אָיִנְיָם אָיִנְיָם אָיִנְיָם אָיִנְיָם אָיִנְיָם אָיִנְיָם אָיִנְיָם אָיִנְיָם	מַּוֹנְמִי בְּיִם וֹלְיִנְּטִּ		Modified aite	MONTH	מייי ביייי ביייי ביייי בייייי בייייי בייייי בייייי ביייייי	MOGILIEG-BICE	WO9219248-A1.	12-NOV-1992.	01-MAY-1992;	03-MAY-1991;	(UNIW ) UNIV W	Stahl PD;	WPI; 1992-398516/48	New high affin mediated by ma infectious dis	Claim 3; Page	This compound represents a binding of labelled mannosy receptors are uniquely four discoportides such as this specifically, to image, lake specifically, to image, lake and used to purify mannose useful in the treatment of secretory products eg. Crob macrophages harbour replications viral infections ilysosomal storage diseases, eg. Gaucher's disease; eg. Gaucher's disease;
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Query Match
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      lose, fucose, glucose or N-Ac-
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                                                                                                                                                                                                                                      non interfering substits."
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Modified-site
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fusion nucleic acid library; scaffold protein; bioactive peptide; phenotype change; cell morphology; cell growth; cell viability; cell adhesion; cellular density; cancer; tumour; apoptosis; cell death; loss of cell division; decreased cell growth; brca-1; brca-2; tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC; brosophila discerlarge, DIg; cardiovascular; neurobiology; bone biology; skin biology; cosmeceutical; endocrinology; infectious disease; drug toxicity; drug resistance; inflammation; allergic response. 20-JUN-2002; 2002US-00177725. US2003143562-A1. 08-OCT-1998; 31-JUL-2003. Synthetic.

Structurally biased random peptide library related protein segid 53.

(first entry)

29-JAN-2004

ADE10646;

98US-00169015. 99US-00415765. 08-OCT-1999;

(RIGE-) RIGEL PHARM INC.

Bogenberger JM; Peelle BR, Anderson D,

WPI; 2003-829786/77

Novel library of fusion nucleic acids each of which has fused first and second nucleic acids encoding scaffold protein and library peptide having alpha helical biasing sequence, respectively, useful in screening methods.

Example 6; SEQ ID NO 53; 110pp; English.

The invention describes a library (I) of fusion nucleic acids, where each fusion nucleic acid comprises a first nucleic acid (NI), encoding a scaffold protein sequence; and a second nucleic acid (NI), encoding a library peptide sequence comprising an alpha helical biasing sequence; where NI is fused to NI. Disclosed is a method for screening bioactive peptides conferring a change in specific phenotype such as cell morphology, cell growth, cell viability, adhesion to substrates or other morphology, cell growth, cell viability, adhesion to substrates or other RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes in the equilibrium state (i.e., half-life) or one or more RNAs, protein, lipids, hormones, cytokines, or other molecules; etc. The bioactive lipids, hormones, cytokines or other molecules, etc. The bioactive peptide identified by above mentioned method is used to generate more candidate peptides and to identify target molecules, i.e., the molecules

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combined with other pharmacologic activators to study the epistatic relationships of signal transduction pathways in question. The disclosed method is also useful in cancer applications. Random libraries can be introduced into any tumour cell (primary or cultured), and peptides call death, loss of division or decreased cell growth. The method is also useful for screening of bioactive peptides which restore the constitutive function of the brca-1 or brca-2 genes, and other tumour suppressor genes of the brca-1 or brca-2 genes, and other tumour suppressor genes important in breast cancer such as the adenomatous polyposis coli gene (APC) and the Drosophila disca-large gene (Ing), which are components of cell-cell junctions. The methods are useful in cardiovascular applications, neurobiology applications, bone biology applications, skin biology applications, cosmeceutical applications, endocrinology applications, immunobiology, inflammation, and allergic response applications, immunobiology, inflammation, and allergic response applications, immunobiology, inflammation, and allergic response applications, immunobiology applications. The peptide clibrary can easily be monitored, both for its presence within cells and tractured cellular concentration of peptides having a given structural bias and thus increase the hit rate for targets that bind such structural and allergic structures. This is the manino acid sequence of a protein associated with structures.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fusion nucleic acid library; fusion protein library; scaffold protein; green fluorescent protein; GFP; alpha helical biasing sequence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 EKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAAK
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with which the bloactive peptide interacts. The peptide(s) can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                 fused nucleic acid and random peptide libraries of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 26.8%; Score 98; DB 7; Length 75; 1 Similarity 44.3%; Pred. No. 0.052; 31; Conservative 11; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleating sequence-containing library fusion protein #47
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08-OCT-1999; 99US-00415765.
20-JUN-2002; 2002US-00177725.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 AAAKEAAYEA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 AAAEAAAKAA 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ANDE/) ANDERSON D. (PEEL/) PEELLE B R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JS2003224412-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 75 AA;
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Matches
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                                                                                              The invention comprises a library of fusion nucleic acids, where each encoded protein contains a scaffold protein (e.g. a green fluorescent protein - GFP) and a library peptide sequence comprising an alpha helical biasing sequence, or a scaffold protein, a library peptide and a nucleating sequence. The library of the invention is useful for screening bloactive peptides conferring a particular phenotype. The present amino acid sequence represents a library protein containing a nucleating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa cells. The SENPs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                 8 EKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAAK 67
                                                                                                                                                                                                                                                                                                                                                                                29
Library of fusion polypeptides in which each polypeptides comprises scaffold protein and library peptide having alpha helical biasing sequence, or scaffold protein, library peptide and nucleating sequence.
                                                                                                                                                                                                                                                                                                                                                                     Peptide #3822 encoded by probe for measuring cervical gene expression.
                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                gene expression in human cervical epithelial cells
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                                                                  Example 6; SEQ ID NO 53; 110pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM17388 standard; protein; 71 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00633366.
21-SEP-2000; 2000US-0234687P.
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04-OCT-2000; 2000GB-00024263.
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60 AAREAAKAA 69
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                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cervical cancer
                                                                                                                                                                                                                                                    Sequence 75 AA;
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The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                                                                                                                           2 KKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAA 56
                                                                                                                                                                                                                                                                                Peptide #3912 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 27; SEQ ID NO 29041; 639pp + Sequence Listing; English.
                                                                                                                                                                                 Score 93; DB 4; Length 71;
Pred. No. 0.14;
8; Mismatches 24; Indels
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20-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-006032368.
03-AUG-2000; 2000US-00632368.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359F.
04-OCT-2000; 2000US-0236359F.
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                                                                                                                                                                                    25.4%;
41.8%;
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Best Local Similarity 41.89
Matches 23, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                Sequence 71 AA;
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Gaps

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Query Match 25.4%; Score 93; DB 4; Length 71; Best Local Similarity 41.8%; Pred. No. 0.14; Matches 23; Conservative 8; Mismatches 24; Indels

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1: \cgn2_6/ptodata/1/pubpaa/PCT_PUBCOMB.pep:*
2: \cgn2_6/ptodata/1/pubpaa/PCT_PWEW_PUB.pep:*
3: \cgn2_6/ptodata/1/pubpaa/PCT_BWEW_PUB.pep:*
4: \cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
5: \cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
6: \cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
7: \cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
8: \cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
9: \cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
10: \cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
11: \cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
12: \cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
13: \cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
13: \cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
14: \cgn2_6/ptodata/1/pubpaa/USIOP_PUBCOMB.pep:*
15: \cgn2_6/ptodata/1/pubpaa/USIOP_PUBCOMB.pep:*
16: \cgn2_6/ptodata/1/pubpaa/USIOP_PUBCOMB.pep:*
17: \cgn2_6/ptodata/1/pubpaa/USIOP_PUBCOMB.pep:*
18: \cgn2_6/ptodata/1/pubpaa/USIOP_PUBCOMB.pep:*
19: \cgn2_6/ptodata/1/pubpaa/USIOP_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-816-989A-5

US-09-816-989A-4

7 US-10-792-311-4

US-09-816-989A-3

US-09-816-989A-3

US-09-816-989A-2

7 US-10-792-311-2

6 US-10-67-004-20

US-09-816-989A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-792-311-1
US-10-390-472-16
US-10-038-854-235
                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                        1465611 seqs, 345679903 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Listing first 45 summaries
                                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
Match Length DB
                                                                                                                                                                                                              US-10-792-311-5
366
                                                                                                                                                                                                                                                                                                                                                                                                                                                               length: 0
length: 77
                                                                                                                              June
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq
Maximum DB seq
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282.5
282.5
245.5
245.5
245.5
131
131
111.5
104.5
101.5
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Perfect score:
                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database
                                                                                                                                6
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No.
                                                                                                                              Run
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RESULT 1154 6 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	14 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1011 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	17.6 17.6 17.6 17.6 17.6 17.6 17.6 17.6 18.6 18.6 18.6 18.6 18.6 18.6 18.6 18.6 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0 19.0	Sequence Seq	236, App 237, App 237, App 237, App 237, App 23, App 196600, 148739, 148739, 164544, 185175, App 100,	Σ H
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Sequence 0-139-49-239 Sequence 0-137-963-19660 Sequence 0-137-963-19660 Sequence 0-137-963-129571 Sequence 0-1393-49-100 Seque	0-038-854-236 Sequence 236, App 0-038-854-239 Sequence 237, App 0-038-854-239 Sequence 237, App 0-038-854-239 Sequence 237, App 0-038-449-53 Sequence 53, App 0-0424-599-144534 Sequence 196600, 0-437-963-196600 Sequence 196600, 0-437-963-196600 Sequence 196600, 0-437-963-129571 Sequence 19600, 1-437-963-129571 Sequence 19600, 1-437-963-129571 Sequence 19600, 1-437-963-129571 Sequence 129571, 0-424-599-238149 Sequence 129571, App 0-393-449-103 Sequence 13973, 1-424-599-238149 Sequence 10, App 0-393-449-103 Sequence 10, App 0-393-449-103 Sequence 10, App 0-393-449-103 Sequence 10, App 0-393-449-103 Sequence 10, App 0-424-599-149912 Sequence 10, App 0-424-599-227076 Sequence 151241 Sequence 151241 Sequence 151241 Sequence 151241 Sequence 151241 Sequence 27076, 0-424-599-278231 Sequence 27026, 0-424-599-278231 Sequence 27026, 0-424-599-278231 Sequence 60, App 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Sequence 3, Application US/09816989A
Sequence 3, Application US/09816989A
Patent No. US20020115103A1
GENERAL INFORMATION:
GENERAL INFORMATION:
THILE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKE
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT PLING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKA
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKA
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REPERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/10/792,311
CURRENT APPLICATION NUMBER: US/09/816,989
PRIOR PILING DATE: 2001-03-23
PRIOR FILING DATE: 1998-09-25
PRIOR PILING DATE: 1998-09-25
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATCHIN VETSION 3.1
SEQ ID NO 4
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                        1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAK 60
                                                           1 AKKYAKKEKAYAK-----AKKAEAK------AAKKAKAEAKKYAKAAKAEKKEYAAABAK 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-10-792-311-4
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Pred. No. 1e-17;
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                                                                                                                                                                                                                                                                                                           ; Sequence 4, Application US/10792311; Publication No. US20050038233A1; GENERAL INFORMATION:
                                                                                                                             77
                                                                                                                                                                              50 YKAEAAKAAKEAAYEA 66
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Best Local Similarity 84.4%;
Matches 65; Conservative
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                                                                                                                               61 YKAEAAKAAAKEAAYEA
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                                                                                                                                                                                                                                                             RESULT 4
US-10-792-311-4
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LENGTH: 56
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TITLE OF INVENTION: AND FOR THERAPEUTIC USE
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REPERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989
PRIOR APPLICATION NUMBER: 00/10,693
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATCHIN OFFICE 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATCHIN VERSION 3.1
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TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFRENCE: 2609/60807-A-PCT-US
FILE REFRENCE: 2609/60807-A-PCT-US
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 4
LENGTH: 66
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US-10-792-311-5
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84.4%; Pred. No. 1e-17;
tive 0; Mismatches 1;
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Pred. No. 7.1e-25;
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Patent No. US20020115103A1
                                                                                                                     Sequence 5, Application US/10792311
Publication No. US20050038233A1
CENERAL INFORMATION:
APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 77; Conservative 0
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APPLICANT: Gad, Alexander
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Best Local Similarity
Matches 65; Conserv
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TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKE
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
THE REFERENCE: 2609/60807-A-PCT-US
CURRENT PAPLICATION NUMBER: US/09/816,989
PRIOR FILING DATE: 2001-03-23
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTI ON NUMBER: PCT/US99/22402
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
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                                                                                                                                                                                                       ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
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Pred. No. 9.3e-05;
0; Mismatches 6; Indels
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Pred. No. 9.3e-05;
0; Mismatches 6
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Sequence 20, Application US/10667004
Publication No. US/0040126820A1
GENERAL INFORMATION:
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Publication No. US20050038233A1
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ORGANISM: Artificial Sequence
                        NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO.
LENGTH: 45
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Best Local Similarity 50.6%;
Matches 39; Conservative
                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
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PRIOR FILING DATE: 1999-09-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: INTEL CORPORATION
APPLICANT: CHAN, Selena
APPLICANT: SU, Xing
                                                                                                                                                                                                                                                                                                                                         39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Gad, Alexander
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                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                         Matches
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APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT PILING DATE: 1998-09-23
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1998-09-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
TITLE OF INVENTION: 2.004/0.002

CURRENT APPLICATION NUMBER: US/09/816,989

PRIOR APPLICATION NUMBER: 60/101,633

PRIOR FILING DATE: 2001-03-23

PRIOR FILING DATE: 1998-09-25

PRIOR FILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PARENTE PARENTE NOS: 7

LENGTH: 56
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                                                                                                                                                                                                          1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAK 60
                           ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 67.1%; Score 245.5; DB 17; Length 56; Best Local Similarity 72.7%; Pred. No. 1.4e-14; Matches 56; Conservative 0; Mismatches 0; Indels 21; Gaps
                                                                                                                                                            Gaps
                                                                                                         Length 56;
                                                                                                                                                            Indels
                                                                                                                                                                                                                                        1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKK-----
                                                                                                   Query Match 67.1%; Score 245.5; DB 9; Best Local Similarity 72.7%; Pred. No. 1.4e-14; Matches 56; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/10792311 Publication No. US20050038233A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                 40 YKAEAAKAAAKEAAYEA 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gad, Alexander APPLICANT: Lis, Doris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JS-09-816-989A-2
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TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: STABLE MACROSCODIC MEMBRANES FORMED BY SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 104.5; DB 17; Length 35; Pred. No. 0.014;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/390,472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AKKYAKKEKAAKKAY---KKEAKAKAAEAAAKEAAYEA 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Mismatches
                   TILLE OF INVENTION: AND FOR THERAPEUTIC USE FILE REFERENCE: 2609/60807-A-PCT-US CURRENT APPLICATION NUMBER: US/10/792,311 PUIOR PLING DATE: 2004-03-02 PRIOR APPLICATION NUMBER: US/09/816,989 PRIOR FILING DATE: 2001-03-23 PRIOR APPLICATION NUMBER: 60/101,693 PRIOR PRILING DATE: 1998-09-25 PRIOR PLING DATE: 1998-09-25 PRIOR PLING DATE: 1999-09-24 PRIOR FILING DATE: 1999-09-24 PRIOR FILING DATE: 1999-09-24 SOFTWARE: PATENTIN VERSION 3.1 SOFTWARE: PATENTIN VERSION 3.1 SEQ. ID NO.1 SEC. 10 NO.2 SEC. 10 NO.1 SEC. 10 NO.1 SEC. 10 NO.1 SEC. 10 NO.1 SEC. 10 NO.2 SEC. 10 NO.1 SEC. 10 NO.1 SEC. 10 NO.1 SEC. 10 NO.1 SEC. 10 NO.2 SEC. 10 NO.1 SEC.
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APPLICATION NUMBER: US/08/293,284
FILING DATE: 22-5402-1994
APPLICATION NUMBER: 07/973,326
FILING DATE: 28-DEC-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
US-10-390-472-16
; Sequence 16, Application US/10390472
; Publication No. US20040087013A1
; GENERAL INFORMATION:
APPLICANT: Holmes, Todd
Zhang, Shuguang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rich, Alexander
DiPersio, C. Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Two Militia Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 17-Mar-2003
CLASSIFICATION: 435
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
28.6%;
Best Local Similarity 65.8%;
Matches 25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-792-311-1
                          TITLE OF INVENTION: CONTROLLED ALIGNMENT OF NANO-BARCODES ENCODING SPECIFIC INFORMATI
TITLE OF INVENTION: SCANNING PROBE MICROSCOPY (SPM)
FILE REPERINCE: INTEL1310-(1914240)
CURRENT APPLICATION NUMBER: US/10/67,004
CURRENT FILING DATE: 2003-09-19
PRIOR PPLICATION NUMBER: US/10/251,152
PRIOR PELING DATE: 2002-09-20
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.1
SEQ ID NO. 20
LENGTH: 63
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TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816, 989A
CURRENT FILING DATE: 1998-09-25
PRIOR FILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR FILING DATE: 1999-09-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.5%; Score 111.5; DB 16; Length 63; 56.2%; Pred. No. 0.0065; tive 0; Mismatches 23; Indels 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEATURE:
OTHER INFORMATION: Synthetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09816989A
Patent No. US20020115103A1
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Publication No. US20050038233A1
GENERAL INFORMATION:
APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
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SOFTWARE: PatentIn version 3.1
SEQ ID NO LEGAL 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial sequence
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Best Local Similarity 56.2<sup>s</sup>
Matches 36, Conservative
YAMAKAWA, Mineo
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Matches 25; Conservative
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APPLICANT: Gad, Alexander
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US-10-038-854-236
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APPLICANT:
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APPLICANT:
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1
                                                                                                                                                                    DB 15; Length 60;
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APPLICANT: Millet, Isabelle
APPLICANT: MacDougall, John R
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-230
                                                                                                                                                               Query Match 27.7%; Score 101.5; DB 15; Length Best Local Similarity 48.3%; Pred. No. 0.045; Matches 29; Conservative 7; Mismatches 23; Indels
                                                                          MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-390-472-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/038,854
CURRENT FILING DATE: 2003-01-22
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PRIOR APPLICATION NUMBER: 60/258,928
PRIOR FILING DATE: 2000-12-29
PRIOR FILING DATE: 2001-01-02
PRIOR FILING DATE: 2001-01-02
PRIOR FILING DATE: 2001-01-04
PRIOR PELING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: 60/269,814
PRIOR APPLICATION NUMBER: 60/269,812
PRIOR APPLICATION NUMBER: 60/279,832
PRIOR FILING DATE: 2001-03-29
PRIOR PILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/279,833
PRIOR APPLICATION NUMBER: 60/279,833
PRIOR APPLICATION NUMBER: 60/279,833
PRIOR APPLICATION NUMBER: 60/279,833
PRIOR PILING DATE: 2001-03-29
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APPLICATION NUMBER: 60/284,447
FILING DATE: 2001-04-18
APPLICATION NUMBER: 60/286,683
PILING DATE: 2001-04-25
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 235, Application US/10038854 Publication No. US20040022781A1 GENERAL INFORMATION:
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PRIOR FILING DATE: 2001-04-13
                        LENGTH: 60 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liu, Xiaohong
Malyankar, Uriel M
Shimkete, Richard A
Tchernev, Velizar
Spaderna, Steven K
Gorman, Linda
Kekuda, Ramesh
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Edinger, Shlomit R
Ellerman, Karen
Gunther, Erik
SEQUENCE CHARACTERISTICS
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Wolenc, Adam R
Vernet, Corine
Eisen, Andrew J
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Gangolli, Esha A
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                                             TYPE: amino acid
TOPOLOGY: linear
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Rastelli, Luca
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APPLICANT:
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3 AKETADSAKEKASEAKDAAKD---KAEBAKDAAKEKAEEAKDKAKEKKAGEAKDKTGNKA 59
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                                                                                                                                                                                                                                                                          Gaps
Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 411 SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 235 LENGTH: 75
                                                                                                                                                                                                                                                                            4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/038,854
CURRENT FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: 60/258,928
PRIOR PILING DATE: 2000-12-29
PRIOR PILING DATE: 2001-01-02
PRIOR APPLICATION NUMBER: 60/259,415
PRIOR PILING DATE: 2001-01-02
PRIOR FILING DATE: 2001-01-04
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/269,814
PRIOR FILING DATE: 2001-03-29
PRIOR PLILING DATE: 2001-03-29
PRIOR PLILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-29
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FILING DATE: 2001-03-29
APPLICATION NUMBER: 60/283,889
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: Spytek, Kimberly A
Iti, Li
: Wolenc, Adam R
: Vernet, Corine
: Bisen, Andrew J
Liu, Xiaohong
Malyankar, Uriel M
Shimkets, Richard A
Spaderra, Steven K
Gorman Iinas
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Edinger, Shlomit R
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Kekuda, Ramesh
Patturajan, Meera
Gusev, Vladimir Y
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Rastelli, Luca
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Gangolli, Esha A
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Boldog, Ferenc
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Gunther, Erik
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                                                                                                                            TYPE: PRT
CORGANISM: Homo sapiens
US-10-038-854-235
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1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKA-EKKEYAAAEA 59
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                                             PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/286,683
PRIOR FILING DATE: 2001-04-25
PRIOR FILING DATE: 2001-04-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 411
SOFTHARE: Patentin Ver. 2.1
LENGTH: 75
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APPLICANT: Gunther, Erik
APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: MacDougall, John R
ITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
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CURRENT FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: 60/289,928
PRIOR FILING DATE: 2000-12-29
PRIOR PLICATION NUMBER: 60/259,415
PRIOR APPLICATION NUMBER: 60/259,785
PRIOR PLILING DATE: 2001-01-02
PRIOR APPLICATION NUMBER: 60/269,785
PRIOR FILING DATE: 2001-01-04
PRIOR FILING DATE: 2001-02-20
PRIOR FILING DATE: 2001-02-20
PRIOR FILING DATE: 2001-02-20
PRIOR FILING DATE: 2001-02-20
FILING DATE: 2001-04-13
APPLICATION NUMBER: 60/284,447
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Publication No. US20040022781A1
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Wolenc, Adam R
Vernet, Corine
Eisen, Andrew J
Liu, Xiaohong
Malyankar, Uriel M
Shimkets, Richard A
Tchernev, Velizar
Spaderna, Steven K
Gorman, Linda
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Edinger, Shlomit R
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Shenoy, Suresh G
Rastelli, Luca
Casman, Stacie J
Boldog, Ferenc
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Busev, Vladimir Y
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                                                                                                                                                                                                                                           TYPE: PRT
CRGANISM: Homo sapiens
US-10-038-854-236
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Sequence 5, Application US/09816989A
Batent No. 6800287
GENERAL INFORMATION:
APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKI
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT FILING DATE: 2001-03-23
RIOR APPLICATION NUMBER: 60/101,693
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR PLILNG DATE: 1999-09-25
PRIOR FILING DATE: 1999-09-24
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                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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Sequence 3
Sequence 3
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/cgm2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgm2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgm2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgm2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                  OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum Match 10
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Match Length DB
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366
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Maximum DB seq length: 77
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13, Appl
16, Appl
16, Appl
17, Appl
11, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 366; DB 4;
100.0%; Pred. No. 7.8e-28;
tive 0; Mismatches 0;
US-08-460-971A-60
US-08-462-040-60
US-08-303-025-13
US-08-313-025-13
US-08-303-025-16
US-08-303-025-16
US-08-303-025-16
US-08-13-4790
US-08-152-488-12
US-08-303-025-14
US-08-303-025-14
US-08-152-488-10
US-08-152-488-10
US-08-152-488-11
US-08-152-488-11
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FEATURE:
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Best Local Similarity 100.
Matches 77; Conservative
  233.5
233.5
233.1
233.1
223.1
223.1
223.1
221.7
221.7
221.6
221.6
221.6
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Sequence 3, Application US/09816989A

Patent No. 6800287

Patent No. 6800287

APPLICANT: Gad, Alexander

APPLICANT: Lis, Doris

TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKI

TITLE OF INVENTION: AND FOR THERAPEUTIC USE

TITLE OF INVENTION: AND FOR THERAPEUTIC USE

TITLE REFERENCE: 2609/60807-A-PCT-US

CURRENT PAPLICATION NUMBER: 00/99/816,989A

CURRENT FILING DATE: 2001-03-23

PRIOR FILING DATE: 1998-09-25

PRIOR FILING DATE: 1998-09-24

PRIOR FILING DATE: 1999-09-24
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                                                                                                                                                                                            ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-4
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Patent No. 6514938
GENERAL INFORMATION:
APPLICANT: Yead Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 56
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OTHER INFORMATION: PEPTIDE
US-09-405-743A-3
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Pred. No. 4.5e-20;
0; Mismatches 1;
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                            SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 66
                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                             Query Match 77.2%;
Best Local Similarity 84.4%;
Matches 65; Conservative
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  NUMBER OF SEQ ID NOS: 7
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APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
APPLICANT: Lia, Doria
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
TILE REPRENCE: 2609/60007—4-DCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT PILING DATE: 1090-103-23
PRIOR FILING DATE: 1098-09-25
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR APPLICATION NUMBER: PCT/US99/22402
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                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
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TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REPERBERGE: 60807-A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 66
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                                                                                                                                                                                                                                                                          Length 77;
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                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%; Pred. No. 7.8e-28;
Matches 77; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09405743A
Patent No. 6514938
GENERAL INFORMATION:
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Patent No. 6800287
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                          SOFTWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 77
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                                                                                                                                  ORGANISM: Artificial Sequence FEATURE:
NUMBER OF SEQ ID NOS: 7
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1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAK 60
                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-2
                                                                                                                                                                                                                                                                                                                  Gaps
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Pred. No. 4.8e-06;
0; Mismatches 6; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,008A
FILING DATE: 18-DEC-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032,436
FILING DATE: 18-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   1 AKKYAKK-----AKAEKA-----KKAYKAAEAKKAAKYE-
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APPLICANT: Karr, Joan F.
APPLICANT: Pohl, Jan
TITLE OF INVENTION: Polycationic Oligomers
UNMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Greenlee, Winner and Sullivan
5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6. Application US/08993008A Patent No. 6153596 GENERAL INFORMATION:
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REGISTRATION NUMBER: 32,064
REFERENCE,DOCKET NUMBER: 33
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 -KAAAEKAAAKEAAYEA 45
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TOPOLOGY: not relevant
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Petros, John A.
     NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                            Query Match 35.8%;
Best Local Similarity 50.6%;
Matches 39; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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US-08-993-008A-6
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APPLICANT: Gad, Alexander

APPLICANT: Gad, Alexander

APPLICANT: Gad, Alexander

APPLICANT: Gad, Alexander

APPLICANT: Gad, Dorie

TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK

TITLE OF INVENTION: AND FOR THERAPEUTIC USE

FILE REFERENCE: 2609/60807-A-PCT-US

CURRENT FILING DATE: 2001-03-23

PRIOR APPLICATION NUMBER: 60/101,693

PRIOR APPLICATION NUMBER: 60/101,693

PRIOR APPLICATION NUMBER: PCT/US99/22402

PRIOR FILING DATE: 1999-09-24
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                                                                                                                                                                                                                                                                                                                                                                                                                     --AEAK 39
                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-3
                                                                                                                                                                                                                                                                                                                  21; Gaps
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US-09-405-743A-2
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TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REPERRENCE: 60807-A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SEGTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 45
                                                                                                                                                                                                                                                          Score 245.5; DB 4; Length 56;
Pred. No. 1.1e-16;
0; Mismatches 0; Indels 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09405743A Patent No. 6514938 GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 56
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Best Local Similarity 72.7%;
Matches 56; Conservative (
                                                                                                           TYPE: PRT ORGANISM: Artificial Sequence
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60807-A
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Best Local Similarity
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Best Local Similarity
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                                                        9 KAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEA 65
                                                                                Gaps
                        1; Gaps
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Patent No. 6514938
GENERAL INFORMATION:
APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 48;
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                      Indels
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  Pred. No. 7.1e-05; 6; Mismatches 17
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                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Polycationic Oligomers
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Mismatches
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APPLICATION NUMBER: US/08/993,008A
FILING DATE: 18-DEC-1997
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032,436
FILING DATE: 18-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                          Sequence 5, Application US/08993008A Patent No. 6153596 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Sullivan, Sally A.
REGISTRATION NUMBER: 32,064
REFERENCE/DOCKET NUMBER: 33-95
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-499-8080
TELEFAX: 303-499-8089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPDy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                  APPLICANT: Liotta, Dennis C.
APPLICANT: Petros, John A.
APPLICANT: Wey, Shiow-Jyi
APPLICANT: Karr, Joan F.
APPLICANT: Pohl, Jan
57.9%;
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                    33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 48 amino acids
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  Best Local Similarity
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Matches 29; Conserv
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                    Matches
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Sequence 1, Application US/09816989A

| Sequence 1, Application US/09816989A
| Patent No. 6800287
| GENERAL INFORMATION:
| APPLICANT: Gad, Alexander
| APPLICANT: Lis, Doris
| TITLE OF INVENTION: AND FOR THERAPEUTIC USE
| TITLE OF INVENTION: AND FOR THERAPEUTIC USE
| FILE REFERENCE: 2609/60807-A-PCT-US
| FILE REPERENCE: 2609/60807-A-PCT-US
| PRIOR PILING DATE: 1998-09-25
| PRIOR PILING DATE: 1999-09-24
| NUMBER OF SEQ ID NOS: 7
| SEQ ID NO 1
| SEQ ID NO 1
| LENGTH: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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APPLICANT: Zhang, Shuguang
APPLICANT: Lockshin, Curtis
APPLICANT: Rich, Alexander
APPLICANT: Holmes, Todd
TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
TITLE OF INVENTION: THEREPOR
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                      Score 104.5; DB 4; Length 35;
Pred. No. 0.0011;
4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28.6%; Score 104.5; DB 4; Length 35;
65.8%; Pred. No. 0.0011;
tive 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Description of Artificial Sequence; ; OTHER INFORMATION: PEPTIDE US-09-405-743A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
CURRENT APPLICATION NUMBER: US/09/405,743A CURRENT FILING DATE: 1999-09-24 SOF SEQ ID NOS: 7 9 SOFTWARE: Patentin Ver. 2.1
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Patent No. 5670483
                                                                                                                                                                                                                                                                                                                                                                         28.6%;
                                                                                                                SEQ ID NO 1
LENGTH: 35
TYPE: PT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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us-10-792-311-5.rai

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NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REGISCOMUNICATION NUMBER: MIT-6008A
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 861-9540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16, Application US/08898300
Patent No. 6548630
GENERAL INFORMATION:
APPLICANT: Zhang, Shuguang
APPLICANT: Rich, Alexander
APPLICANT: Holmes, Todd
TITLE OF INVENTION: STABLE MACROSCO;
TITLE OF INVENTION: SLEF-ASSEMBLY OF TITLE OF INVENTION: THEREFOR NUMBER OF SEQUENCES: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (781) 861-9540
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein US-08-293-284A-16
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
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Sequence 16, Application US/08293284A

Patent No. 595543

GENERAL INPORMATION:
APPLICANT: Chang, Shuguang
APPLICANT: Chang, Shuguang
APPLICANT: DiPersio, C. Michael
APPLICANT: Lockshin, Clurtis
TITLE OF INVENTION: SELE-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
TITLE OF INVENTION: THEREFOR
INTERTION: THEREFOR

NUMBER OF SEQUENCES: 64

CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.7%; Score 101.5; DB 1; Length 60; 48.3%; Pred. No. 0.0037; tive 7; Mismatches 23; Indels
                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,849
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,284A
FILING DATE: 22-AUG-1994
                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,326
FILING DATE: 28 DECEMBER 1992
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: MIT-6008.
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,326
Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 48.33
Matches 29; Conservative
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STATE: Massachusetts
                         Lexington
Massachusetts
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                                                                COUNTRY: U.S.A.
ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-293-284A-16
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2 KKYAKKEKAYAKKAEKAAK-KAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAK 60
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SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
THEREFOR
Query Match 27.7%; Score 101.5; DB 2; Length 60; Best Local Similarity 48.3%; Pred. No. 0.0037; Matches 29; Conservative 7; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILION, BROOK, SMITH & REYNOLDS, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALDERSES.

ALDERSES.

ALDERSES.

CITY: Lexington
STREET: Two Militia Drive
CITY: Lexington
STREET: Massachusetts
COUNTRY: U.S.A.

ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: BACHOIL NELSES #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/898,300
FLING DATE: 22 JULY 1997
CLASS!FICATION NUMBER: 08/346,849
FLING DATE: 30 NOVENBER 1994
PRIOR APPLICATION NUMBER: 07/973,326
FLING DATE: 28 DECEMBER 1994
PRIOR APPLICATION NUMBER: 22 DECEMBER 1992
ATTORNEY/AGENT INFORMATION:
NAME: Brock, David E.
REFERENCE/DOCKET NUMBER: MIT-6008FB
TELERCOMMUNICATION INFORMATION:
TELERCOMMUNICATION INFORMAT
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US-08-898-300-16

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2 KKYAKKEKAYAKKAEKAAK-KAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAK 60
                                                                                                                           Query Match 27.7%; Score 101.5; DB 4; Length 60; Best Local Similarity 48.3%; Pred. No. 0.0037; Matches 29; Conservative 7; Mismatches 23; Indels 1; Gaps
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Search completed: June 3, 2005, 11:17:01 Job time: 41 secs

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                                                                                                                                                                                                                                                   1 AKKYAKKEKAYAKKAEKAAK......KKAYKAEAAKAAAKEAAYEA
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                             283416 segs, 96216763 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Match Length
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1: pir1:*
2: pir2:*
3: pir3:*
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length: 86
                                                                                                                             June
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Perfect score:
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                                                                                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                                                                                                             Searched:
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No.
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30 57 13.9 64 2 T22415  31 57 13.9 64 2 A6457  32 56.5 13.8 84 2 AB1629  34 56.5 13.8 84 2 AB1629  35 56.5 13.8 84 2 AB1629  36 55.5 13.6 64 2 S64536  38 55.5 13.6 64 2 S64536  39 55.5 13.6 64 2 S64536  39 55.5 13.6 67 2 S64516  41 54.5 13.3 67 2 S64516  42 54 13.2 51 2 S6760  43 55 13.4 67 2 S6760  44 54 13.2 51 2 A63711  44 54 13.2 51 2 A63711  45 54 13.2 51 2 A63711  46 54 13.2 51 2 A63711  ALIGNMENTS  RESULT 1  ALREADER COULTING HEAD LIDERAY, AUGUST 1999 #LEXX_Ch6_CfSpecies : Generalbadditis elegans CfSpecies: General protein COIBIO.5 - Caenorhabditis elegans CfSpecies: Caenorhabditis Conservative SfSpecies: Caenorhabditis Conservative CfSpecies: Caenorhabditis Conservative CfSpecies: Caenorhabditis Conservative CfSpecies: Caenorhabditis elegans CfSpecies: Caenorhabditis Caenorhabditis CfSpecies: Caenorhabd	hypothetical prote archaeal histone - hypothetical prote ribosomal protein ribosomal protein histone Hi.b. hepa myosin heavy chain ribosomal protein artifreeze protein archaeal histone - hypothetical protee M protein precurso collagen alpha 1(X archaeal histone - histone HMRA2 - Me hypothetical prote	ALIGNMENTS . orhabditis elegans	-Oct-1 cosmi /EMBL/	: IV 3; 61/3 5. 20.0%; Score 82; DB 2; Length 62; imilarity 43.6%; Pred. No. 7.4; ; Conservative 5; Mismatches 24; Indels 2; Gaps 1; AKKYAKKEKAYAKKAEKAAKAAEAKAYKAAEAKKKAKAAEAKKYAKAEKAE 53	r (Holothuria tubulosa) 28-Peb-1990 #text_change 09-Jul-2004 1lo, A. for phi(0), a histone to protamine transition prot 74; PMID:2602115	ore 81; DB 2; Length 78; d. No. 10; Mismatches 18; Indels 12; Gaps 3;
30 57 13.9 64 2 31 57 13.9 67 2 32 56.5 13.8 84 2 34 56.5 13.8 84 2 34 56.5 13.8 84 2 35 56 13.7 79 2 36 55.13.8 84 2 37 55.5 13.6 64 2 39 55.5 13.6 62 2 40 55.5 13.6 62 2 41 54.5 13.3 60 2 42 54 13.2 68 2 43 55.5 13.6 68 2 44 54 51 13.2 67 2 44 54 13.2 67 2 45 64 13.2 67 2 46 65 67 2 48 66 67 2 49 67 2 49 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68 2 40 68	T22415 A64451 T02461 AH1259 AB1022 AB1023 S5156 D64416 G87600 S60803 A64321 A64321 A64321	ALIC	vision 2 ry, Augurelegar d from G	Score Pred. 5; Mit AKKAEAKI   :	cucumber vision ( z-Carril 89 a CDNA ( :900987'	Scc Pre 19;
30 57 13.9 64 31 57 13.9 67 32 5.5 13.8 84 34 56.5 13.8 84 34 56.5 13.8 84 34 56.5 13.8 84 34 56.5 13.6 64 37 55.5 13.6 67 37 55.5 13.6 82 38 55.5 13.6 82 40 55.5 13.4 67 41 54.5 13.2 68 42 54 13.2 68 43 55.5 13.4 67 44 54.5 13.3 60 42 55.1 13.2 68 44 54 13.2 67 44 54 13.2 67 44 54 13.2 67 45 54 13.2 67 47 55.5 13.6 67 48 54 13.2 68 48 51 13.2 68 48 51 13.2 68 48 51 13.2 68 48 51 13.2 68 48 51 13.2 68 48 51 13.2 68 48 51 13.2 68 48 51 13.2 68 48 51 13.2 68 48 51 13.2 68 48 51 13.2 68 48 51 13.2 68 48 68 68 68 68 48 68 68 68 68 48 68 68 68 68 48 68 68 68 68 48 68 68 68 68 48 68 68 68 68 48 68 68 68 68 48 68 68 68 68 48 68 68 68 68 48 68 68 68 68 48 68 68 68 68 48 68 68 68 68 48 68 68 68 68 48 68 68 68 68 48 68 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 68 48 68 68 48 68 68 48 68 68 48 68 68 48 68 68 48 68 68 48 68 68 48 68 68 48 68 68 48 68 68 48 68 68 48 68 68 48 68 68 48 68 68 48 68 68 48 68 68 48 68 68 48 68 68 48 68 68 48 68 68 48 68 68 48 68 68 48 68 68 48 68 68 48 68 68 48 68 68 48 68 68 48 68 68 48 68 68 48 68 68 48 68 68 48 68 68 48 68 68 48 68 68 48 68 48 68 48 68 48 68 48 68 48 68 48 68 48 68 48 68 48 68 48 68 48 68 48 6	0000000000000000	i	Jan re F C	68; BKA A	ea a Lre 119 Off UID	80 G
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31 57 113 31 57 113 32 5.5 113 33 5.5 113 34 5.5 113 34 5.5 113 35 5.5 113 37 5.5 113 37 5.5 113 37 5.5 113 37 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39 5.5 113 39	000000000000000000000000000000000000000	9	MBL ZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZ	1/3 arrit	n ph ria 0 ## 177. 177. 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	ari) ons
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RESULT T310 A) ACCESS BY A A CONTROL OF CONT	. 8 & R R R R R R R R R R R R R R R R R R	1 tical pro	22-Oct-1 22-Oct-1 8ion: T3 8ion: T3 hard, M. ed to the iption: T ence num 8ion: T3 8i prelir ule typel ues: 1-6;	icmental in its continuous 27/3 Colbio. Match Local Sines 24;	ding prodes: Holor 28-Feb-18-18-18-18-18-18-18-18-18-18-18-18-18-	Match Local Sines 24;
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82

RESULT 3

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NyAlternate names: neurofilament triplet L protein (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Species: A02964
R;Isobe, T.; Okuyama, T.
FRBS Lett. 182, 389-332, 1985
A;Title: Brain micro glutamic acid-rich protein is the C-terminal endpiece of the neurofi
A;Reference number: A02964; MUID:85154567; PMID:3884373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C,Accession: S10544
R,Ausio, J.; McParland, R.
Bur. J. Biochem. 182, 569-576, 1989
A;Title: Sequence and characterization of the sperm-specific protein phi3 from Mytilus cs
A;Reference number: S04941; MUID:89325302; PMID:2666130
A;Accession: S10544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Comment: This acidic protein, isolated from the cytosolic fraction of brain tissue, cor C;Comment: The similarity of this sequence to part of the neurofilament triplet L proteir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N;Alternate names: protamine PL-IV.2
C;Species: Mytilus californianus (California mussel)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 EAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKKAYKAEAAKAAAKEA
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                                                                                                                                                                                                                                                                                                                                          17.8%; Score 73; DB 1; Length 85; 45.3%; Pred. No. 40; 32; Indels iive 1; Mismatches 32; Indels
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                                   A,Residues: 1-85 <LIN>
A;Cross-references: UNIPROT:P02734
C;Superfamily: antifreeze protein
C;Keywords: antifreeze
F;1-21/Domain: signal sequence #status predicted <SIG>F;22-85/Product: antifreeze protein 4 #status predicted <MAT>
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A;Residues: 1-45 AAUS-
A;Cross-references: UNIRROT:P11860
C;Superfamily: histone H1
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                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 45.3
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Best Local Similarity
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(species: Mytilus californianus (California mussel)

(c)Species: Mytilus californianus (California mussel)

(c)Accession: 810845

(R)Accession: 810846

(R)Accession: 182, 869-576, 1989

(A)Atitle: Sequence and characterization of the sperm-specific protein phi3 from Mytilus A)Reference number: 804941; MUID:89325302; PMID:2666130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: S04941
R;Ausio, J.; McParland, R.
Eur. J. Biochem. 182, 569-576, 1989
A;Title: Sequence and characterization of the sperm-specific protein phi3 from Mytilus A;Reference number: S04941; MUID:89325302; PMID:2666130
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R; Lin, Y.; Gross, J.K.
Proc. Natl. Acad. Sci. U.S.A. 78, 2825-2829, 1981
A; Title: Wolecular cloning and characterization of winter flounder antifreeze cDNA. A; Reference number: A03193; WUID:81247379; PMID:6265915
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61
                                                                                                                                                                                                                                                                                                                                                                                  protamine phi-3.1 - California mussel
NiAlbernate names: protamine PL-IV.
C:Species: Mytlius californianus (California mussel)
C:Species: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
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C;Species: Pseudopleuronectes americanus (winter flounder)
C;Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004
10 ARKPAARRESAAKRAAPAAKKAASR--RRPKSAKKAKPAARRRSSVKPKAAK-----AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 76; DB 2; Length 45;
Pred. No. 15;
8; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAK 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAK 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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42.2%; Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Note: 6-Thr, 17-Thr, and 18-Thr was also found C;Superfamily: histone H1
C;Keywords: DNA binding; nucleus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protamine phi-3.3 - California mussel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: UNIPROT: P11860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Cross-references: UNIPROT:P11860
C,Superfamily: histone H1
C,Keywords: DNA binding; nucleus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 44.4%;
Matches 20; Conservative
                                                                                AEAKYKAEAAKKA 69
                                                                                                                                 |: : :: :: AOVRRESERIREA 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: protein A;Residues: 1-45 <AUS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein A; Residues: 1-45 <AUS>
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RESULT 4

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C;Accession: S70831
R;Davis, J.M.; Mayor, J.; Plamann, L.
Mol. Microbiol. 18, 943-952, 1995
A;Title: A missense mutation in rpoD results in an A-signalling defect in Myxococcus xant A;Reference number: S70829; MUID:96422481; PMID:8825098
                                           C;Accession: A02653
R;Watson, D.C.; Wong, N.C.W.; Dixon, G.H.
Eur. J. Biochem. 95, 193-202, 1979
A;Title: The complete amino-acid sequence of a trout-testis non-histone protein, H6, loce A;Reference number: A02653; MUID:79213375; PMID:456349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: G83572
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bri adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, ...; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathoc A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: G83572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:0915V8; GB:AE004494; GB:AE004091; NID:g9946446; PIDN:AAG03968
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30S ribosomal protein S21 PA0579 [imported] - Pseudomonas aeruginosa (strain PAO1) C;Species: Pseudomonas aeruginosa C;Date: 15-Sep_2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ï
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ribosomal protein S21 - Myxococcus xanthus
C;Species: Myxococcus xanthus
C;Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 KKABKAAKKAEAKAYKAAEAKKKAKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKKAYKA
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 30-Sep-1979 #sequence_revision 08-Oct-1981 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 KAYAKKAEKAAKKAEAKAYK-----AAEAKKKAKAEAKKYAKAAKAEKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35; Indels
                                                                                                                                                                                                                                                                 A,Cross-references: UNIPROT:P02315
A,Experimental source: testis
A,Note: this protein was formerly called histone T
C,Superfamily: nonhistone chromosomal protein HMG-17
C,Keywords: chromosomal protein; DNA binding; nucleus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Superfamily: Escherichia coli ribosomal protein S21
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 16.3%; Score 66.5; D
Best Local Similarity 35.7%; Pred. No. 99;
Matches 25; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: nucleic acid sequence not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73 EAAKAAAKEA 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 QAAGDGAGNA 68
                                                                                                                                                                                                                   A; Molecule type: protein A; Residues: 1-69 < WAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-71 <STO>
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Matches
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Nucleic Acids Res. 19, 307-311, 1991
A;Title: Molecular cloning and characterization of the gene encoding the adenine methylt A;Reference number: 826850; MUID:91195052; PMID:2014170
A;Accession: 826850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-81 < WILD-
A;Residues: 1-81 < WILD-
A;Cross-references: UNIPROT: O9XWY9; EMBL: AL032621; PIDN: CAA21493.1; GSPDB: GN00021; CESP:
A;Experimental source: clone Y45F3A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 æ,
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                                                               12 AKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKKAYK 71
                                                                                          3 AIKDKERKERRDKKLAIANLAAKOKREKKKOOKNGAELAARARKAKAEKAKTSEPPAGGV 62
                                                                                                                                                                                                                                                                                                                                                    hypothetical protein Y45F3A.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein A - Chlorella virus CV-XZ6E
C;Species: Chlorella virus CV-XZ6E
C;Date: 09-Jun-1994 #sequence_revision 10-Nov-1995 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
          Gaps
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          4.
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          Indels
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          30;
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6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nonhistone chromosomal protein H6 - rainbow trout
N;Alternate names: histone T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Library, October 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.1%; Score 70; DB 35.9%; Pred. No. 63; tive 12; Mismatches
          Mismatches
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        12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 VTRAAAQKA--REAAQAA 78
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Best Local Similarity 46.0%;
Matches 23; Conservative 6
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Best Local Similarity 35.9%
Matches 28, Conservative
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        Conservative
                                                                                                                                                                 72 AEAAKAAAKE 81
                                                                                                                                                                                                                   EEKKDEGAGE 74
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submitted to the EMBL Data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Reference number: Z20289
A;Accession: T26945
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A;Introns: 27/3; 53/3
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A; Residues: 1-64 < DAV>

Query Match

Best Loca Matches

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A,Cross-references: UNIPROT:Q8Y506, GB:NC_003210, PIDN:CAD00350.1; PID:g16411742, GSPDB:CA;Experimental source: strain EGD-e C;Genetics: Imo2272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q38583; EMBL:X89721; NID:g1052805; PIDN:CAA61871.1; PID:g1057 R;Alonso, J.C.; Luder, G.; Stiege, A.C.; Chai, S.; Weise, F.; Trautner, T.A. Gene 204, 201-212, 1997 A;Title: The complete nucleotide sequence and functional organization of Bacillus subtili A;Reference number: Z22137; MUID:98094274; PMID:9434185
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6
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C;Species: phage SPP1
C;Species: phage SPP1
C;Species: phage SPP1
C;Species: 13-dan-1996 #text_change 09-Jul-2004
C;Accession: SS9143; T42284
C;Accession: SS9143; T42284
R;Becker, B.; Gassel, M.; Tavares, P.; Lurz, R.; Alonso, J.C.
submitted to the EMBL Data Library, July 1995
A;Description: Head morphogenesis of the Bacillus subtilis bacteriophage SPP1.
A;Reference number: SS9137
A;Reference number: SS9137
A;Reference rumber: SS9137
A;Reference rumber: SS9137
A;Residues: 1-58 -BEC>
                                                                                                                                                                                                                                                                                                                                                                   16 EKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKKAYKAE 73
                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                       Query Match 14.9%; Score 61; DB 2; Length 69; Best Local Similarity 34.5%; Pred. No. 2.4e+02; Matches 20; Conservative 7; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 14.7%; Score 60; DB 2; Length 58; Best Local Similarity 39.6%; Pred. No. 2.5e+02; Matches 19; Conservative 7; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Accession: T42284
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DDA
A;Residues: 1-58 <ALO>
A;Cross-references: EMBL:X97918; PIDN:CAA66545.1
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A;Residues: 1-69 <GLA>
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                        A;Cross-references: UNIPROT:P49225; EMBL:U20669; NID:g710339; PIDN:AAB60205.1; PID:g7103
C;Genetics:
A;Gene: Yakone: Sakone: Companies: C;Superfamily: Bscherichia coli ribosomal protein S21
C;Superfamily: Bscherichia coli ribosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Contents: annotation
C; Superfamily: histone H1
C; Keywords: acetylated amino end; chromosomal protein; DNA binding; nucleosome; nucleus;
F; 1/Wodified site: acetylated amino end (Ser) #status experimental
F; 37/Binding site: phosphate (Ser) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: A02579
R;Rall, S.C; Cole, R.D.
J. Biol. Chem. 246, 7175-7190, 1971
A;Title: Amino acid sequence and sequence variability of the amino-terminal regions of A;Reference number: A02578; MUID:72068710; PMID:5167020
A;Accession: A02579
A;Accession: A02579
A;Accession: A02579
A;Residues: 1-73 <RAL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                   9; Gaps
                                                                                                                                                                                                                         Match 15.0%; Score 61.5; DB 2; Length 64; Local Similarity 34.8%; Pred. No. 2.1e+02; Les 23; Conservative 8; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 15.0%; Score 61.5; DB 2; Length 73; Local Similarity 37.3%; Pred. No. 2.3e+02; Mesmatches 25; Conservative 8; Mismatches 27; Indels
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A;Cross-references: UNIPROT:P02252 R;Langan, T.A; Rall, S.C.; Colf, R.D. J. Biol. Chem. 246, 1942-1944, 1971 A;Reference number: A37504; MUID:71134818; PMID:5547708

Query Match

Best Loc Matches

à

8

histone H1.4 - rabbit (fragment)

13

||| |: KKARKS 63 67 KKAYKA 72

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Righaer, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J. Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma A;Authors: Kreft, J.; Kuhn, M.; Title: Comparative genomics of Listeria species.
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                          hypothetical protein lmo2272 [imported] - Listeria monocytogenes (strain EGD-e)
                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
76 KAAAKEA 82
                                                                                               LAALKKA 66
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C; Accession: AH1358

RESULT 14

A; Status: preliminary A; Molecule type: DNA

A; Accession: AH1358

plasmodium holothuria bdellovibri

Q7ri34 Q94582

lactobacill

streptococc bdellovibri pseudopleur rhizobium l

coxiella bu mytilus cal

Q6mgw9 1 P11860 1 Q83e57

oryza sativ oryza sativ

neurospora

Q6mk36 P02734 Q9c2j3 Q98iv3 Q6k9w4

June

Run on:

Perfect score:

Sequence:

Scoring table:

Searched:

Database

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1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAK
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
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Thesis (2000), Department of Parasitology, Institute of Zoology,
SWITZERLAND.
                                                                                                                                                                                                                                                                                                                                                                         Score 116; DB 2; Length 81;
Pred. No. 0.19;
4; Mismatches 33; Indels
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0711Y2
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07S1J3
07S1J3
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Q653G8
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28.4%;
Best Local Similarity 48.8%;
Matches 41; Conservative
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81 AA; 8012 MW;
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                                                                                                                                                                                                                                                                         Name=H1C81; Synonyms=H1B81;
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   SEQUENCE FROM N.A.
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01-OCT-2003 (
01-OCT-2003 (
Histone H1.
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01-OCT-2000 (
05-JUL-2004 (
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                                                                                                                      72.5
 58
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Q9N6L9;
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026907 trypanosoma
096k5 trypanosoma
097k81 pseudomonas
097k81 pseudomonas
097k6 trypanosoma
097k6 trypanosoma
097k6 trypanosoma
097k5 trypanosoma
097k5 trypanosoma
090k677 trypanosoma
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0950k61 trypanosoma
0950k61 trypanosoma
095k10 trypanosoma
095k10 trypanosoma
095k10 trypanosoma
095k10 trypanosoma
095k11 trypanosoma
09111 trypanosoma
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caenorhabdi
caenorhabdi
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chlorobium
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                                                                     3, 2005, 11:17:09 ; Search time 171 Seconds (without alignments) 257.537 Million cell updates/sec
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                                                                                                                                1 AKKYAKGEKAYAKKAEKAAK......KKAYKAEAAKAAAKEAAYEA
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P14309
Q8kf25
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           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                1612378 segs, 512079187 residues
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0161 TRYCR
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H1C8 TRYCR
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PHI0_HOLTU
Q8KF25
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Maximum Match 100%
Listing first 45 summaries
                                                   OM protein - protein search, using sw model
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Q95UN6
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Q9U3W3
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2: uniprot_trembl:*
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Match Length
                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 86
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Gaps

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9 57

93.5 93.5 89.5

94 96.

111.5 110.5 107.5 104.5 103.5 100.5

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Result

97.5 97.5 97.5 97.5

84.5

81.5

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62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae, Trypanosoma.
NCBI_TaxID=5702;
                                                                                                                                                                                                                                       Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBL_TaxID=5693;
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=89364992; PubMed=2475776; DOI=10.1016/0166-6851(89)90115-1;
Lafaille J.J., Linss J., Krieger M.A., Souto-Padron T., de Souza W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Goldenberg S.,
Structure and expression of two Trypanosoma cruzi genes encoding
antigenic proteins bearing repetitive epitopes.";
Mol. Biochem. Parasitol. 35:127-136(1989).
EMBL, J04016, AAA30177.1;
InterPro; IPR009761; CRA_rpt.
Péan; PF07046; CRA_rpt.
NON TER
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                                                                                                                                026907;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Cytoplasmic repetitive antigen (CRA) protein (Fragment).
Trypanosoma cruzi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=427;
Grueter E., Betschart B.;
Grueter E., Betschart B.;
Submitred (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ287607; CAB76192.1; -.
SEQUENCE 76 AA; 7505 MW; 83BE50D89F1BED8F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Grueter E.;
Thesis (2000), Department of Parasitology, Institute of
SWITZERLAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 AA; 7208 MW; ED6CF031B3DE7D1F CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                68 AA.
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PRT;
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Best Local Similarity 48.8
Matches 40; Conservative
                                                                                                                PRELIMINARY;
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SEQUENCE FROM N.A.
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                         Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBL_TaxID=31285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=H1B76; Synonyms=H1A76;
Trypanosoma brucei gambiense.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Grueter E.,
Thesis (2000), Department of Parasitology, Institute of Zoology,
                                                                                                                                Grueter E.;
Thesis (2000), Department of Parasitology, Institute of Zoology,
SWITZERLAND.
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47.6%; Pred. No. 0.37;
tive 4; Mismatches 34; Indels
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                                                                                                                                                                                                                         STRAIN=1257;
Grueter E., Betschart B.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
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Grueter E., Betschart B.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ2875462; CAB76177.1; -.
EMBL; AJ272462; CAB76172.1; -.
SEQUENCE 76 AA; 7516 MW; 48882064F7B9A6F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                81 AA; 8040 MW; 360FC77DE2E24320 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76 AA.
                                                                                                                                                                                                                                                                            EMBL; AJ272461; CAB76171.1; ...
GO; GO:0000796; Cinucleosome; IEA.
GO; GO:0005634; Cinucleosome; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:000347; P:nucleosome assembly; IEA.
InterPro; IPR00639; Histone_H5.
PRINTS; PR00624; HISTONEH5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 YKAEAAKKA--YKAEAAKAAKEA 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 PKKAAPKKVAPKKVAGKKAAAKKA 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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                 rypanosoma brucei gambiense.
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STRAIN=STIB 755, and 1257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 47.6
Matches 40; Conservative
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                                                                                           SEQUENCE FROM N.A.
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                                                                                                            STRAIN=1257;
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Matches
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Q9N6J8
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Q9N6K0;
01-OCT-2000 (TrEMBLrel. 15, Created)
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01-OCT-2002 (TrEMBLrel.
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01-OCT-2000
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           2 AKASAAPKKAVAKKA-APKKAVAK--KAAPKKAVAKKAAPKKAVAKKAAPKK---AVAK 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAK
                                                                                                                                                                                                           Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBL_TaxID=5702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=DC3000;
MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;
Buell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T.,
                                                                                                                                                                                                                                                                         Grueter E.;
Thesis (2000), Department of Parasitology, Institute of Zoology,
SWITZERLAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas syringae (pv. tomato).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26; Indels
                                                                                                                                                                                                                                                                                                                                STRAIN=TREU 927/4;
Grueter E., Betschart B.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
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Grueter E., Betschart B.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, AJ400880; CAB90837.1; -.
EMBL, AJ28760; CAB76191.1; -.
EMBL, AJ287602; CAB76181.1; -.
SEQUENCE 71 AA; 7019 MW; 406BE51794847C80 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ilarity 51.4%; Score 104.5; D ilarity 51.4%; Pred. No. 1.1; Conservative 4; Mismatches
                                                                                                                        71 AA.
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                                                                                                                                                Created)
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                                           82
                                                                                                                        PRT;
                                                               55 KVAATKPLAKKVAGKKAAKKA 76
                                                                                                                                                                                          Name=H1D71; Synonyms=H1B71, H1C71;
Trypanosoma brucei brucei.
                                           61 YKAEAAKKAYKAEAAKAAAKEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
OrderedLocusNames=PSPTO4673;
                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KVAGKKAAAKKA 71
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01-OCT-2000
                                                                                                                                                                                 Histone H1.
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Matches
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2 AKASAAPKKAVAKKA--APKKAVAK--KAAPKKAVAKKAAPKKAVAKKAAPKKAVA 57
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         Madpu R., Daugherth S.C., Brinkac L.M., Beanan M.J., Haft D.H., Nelson W.C., Davidsen T.M., Zafar N., Zhou L., Liu J., Yuan Q., Rhouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J., Utcrback T.R., Van Aken S.E., Feldhlyum T.V., D'Ascenzo M., Deng W.-L., Ramos A.R., Alfano J.R., Cartinhour S., Chatterjee A.K., Bender C.L., White O., Fraser C.M., Collmer A.; Chneider D.J., Tang X., "The complete genome sequence of the Arabidopsis and tomato pathogen Pseudomonas syringse pv. tomato DC3000.";

Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=H1A71;
Trypanosoma brucei gambiense.
Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=31285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Thesis (2000), Department of Parasitology, Institute of Zoology,
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Durkin A.S., Kolonay J.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 25.3%; Score 103.5; DB 2; Length 82; Best Local Similarity 39.5%; Pred. No. 1.5; Matches 30; Conservative 10; Mismatches 35; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.9%; Score 102; DB 2; Length 71; 48.7%; Pred. No. 1.7;
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Grueter E., Betschart B.;
Submitted (FBB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ287594; CAB76116.1; -
                                                                                                                                                                                                                                                                                                                                                                           Complete proteome; Hypothetical protein.
SEQUENCE 82 AA; 8888 MW; 3826079B39FAD75C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6C7DED4F3E75D8C4 CRC64;
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Last annotation update)
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Trypanosoma brucei brucei.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI TaxID=5702;
                                                                                                                                                                                   Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                                                                                        76 AA.
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                                                                                                                                                                      Created)
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                                                            68 KKVAPK---KVAGKKAAAKKA
                              62 KAEAAKKAYKAEAAKAAAKEA
                                                                                                                                                                   01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-MAR-2003 (TrEMBLrel. 23, Histone H1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 48.1
Matches 39; Conservative
                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AKKYAKKEKAYAKKA--EKAA-KKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAA
                                         Trypanosoma brucei brucei.
Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Histone H1.
Name-H1B85; Synonyms-H1A85;
Trypanosoma brucei gambiense.
Eukaryota: Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=31285;
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8
                                                                                                                                                   Grueter E.; Thesis (2000), Department of Parasitology, Institute of Zoology,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Grueter E.;
Thesis (2000), Department of Parasitology, Institute of Zoology,
SWITZERLAND.
                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.4%; Score 100; DB 2; Length 85; 48.1%; Pred. No. 2.7;
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Pred. No. 2.1;
4; Mismatches 27; Indels
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SEQUENCE FROM N.A.
STRAIN-TREU 927/4;
Grueter E., Betschart B.;
Grueter E., Betschart B.;
Grueter E., Betschart B.;
Grueter E., A44008H1; CRS08039.1;
EMBL; A44008H1; CRS08039.1;
EMBL; A7287600; CAB76185.1;
T. AA; 7005 MW; 478C7B6994847C80 CRC64;
                                                                                                                                                                                                                                STRAIN=TREU 927/4;
Grueter E., Betschart B.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRANTE-STIB 755, and 1257;
Grueter E., Betschart B.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ287591; CAB7613.1; -.
EMBL, AJ272459; CAB76159.1; -.
SEQUENCE 85 AA, 8647 MW; CEEFA3AB5269465E CRC64;
                 Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last annotation update)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence update)
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50.0%;
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01-OCT-2000 (TrEMBLrel. 15,
05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=STIB 755, and 1257;
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Best Local Similarity 50.0°
Matches 36; Conservative
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Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 KVAGKKAAAKKA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 EAKYKAEAAKKA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                      SEQUENCE FROM N.A.
STRAIN=TREU 927/4;
                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                              Histone H1.
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Q9N668; 99N6Q RESULT 10

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1 AKKYAKKEKAYAKKA--EKAA-KKAEAKAYKAAEAKKKAKAEKKYAKAAKAEKKEYAAA 57
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Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5702;
                                                                                                                                                                                                                                                                                                                                         Gaps
Grueter E.;
Thesis (2000), Department of Parasitology, Institute of Zoology,
SWITZERLAND.
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Thesis (2000), Department of Parasitology, Institute of Zoology,
SWITZERLAND.
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                                                                                                                                                                                                                                                                                      Length 76;
                                                                                                                                                                                                                                                                                                                                      29; Indels
                                                                                              SEQUENCE FROM N.A.
STRAIN=TREU 927/4;
Grueter E., Betesvert B.;
Submitted (MAX-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ400880; CAB90836.1; ...
SEQUENCE 76 AA; 7631 MW; 2493E88448B3E0FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=TREU 927/4;
Grueter E., Betschart E.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ208799; CAB76182.1; -.
SEQUENCE 76 AA; 7587 MW; 2959EF4982B2E0F9 CRC64;
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Fri Jun

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54 YAAAEAKYKAEAAKKA
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                                                                                                                                                                                                                        41; Conservative
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                                                                                                                                                                                                    Local Similarity
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  SEQUENCE FROM N.A. STRAIN=Ketri 2693;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3;
                                                                                               2 AKASAAPKKAVAKKAAPKKAAPKKAVAK -- KAAPKKAVAKKAAPKKAVAKKDLAKKVVAK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 EKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAKAEKYAKAAKAEKKEYAAAEAKYKAEAAK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AKKYAKKEKAYAKKA--EKAA-KKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                               Trypanosoma cruzi.
Bukaryota, Buglenozoa, Kinetoplastida, Trypanosomatidae, Trypanosoma.
NCBI_TaxID=5693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein, DNA-binding; Multigene family; Nuclear protein. 80 AA; 8271 MW; 8E83DA508F0A5D31 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=95059220; PubMed=7969272; DOI=10.1016/0166-6851(94)90082-5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aaslund L., Carlsson L., Henriksson J., Rydaaker M., Toro G.C., Galanti N., Pettersson U.;
Ry gene family encoding heterogeneous histone H1 proteins in Trypanosoma cruzi."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29; Indels
                         29; Indels
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 97.5; DB; Pred. No. 3.8; 4; Mismatches
                                                                                                                                                                                                                                                                                                                  80 AA.
      48.1%; Pred. No. 3.6;
                           4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mol. Biochem. Parasitol. 65:317-330(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                           EAKYKAEAAKKAYKAEAAKAA 78
                                                                                                                                                                                                    60 KVAPKKVAGKKA----AAKKA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR005819; Histone H5. PRINTS; PR00624; HISTONEH5.
                                                                                                                                                                                                                                                                                                                                                           01-FEB-1995 (Rel. 31, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 46.7%
Best Local Similarity 48.1
Matches 39; Conservative
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                                                                                                                                                                                                                                                                                                                  STANDARD;
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NCBL_TaxID=5702;
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Thesis (2000), Department of Parasitology, Institute of Zoology,
                                                                                                                                                                          6
                                                                                                                               Length 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23.7%; Score 97; DB 2; Length 76; 52.6%; Pred. No. 3.9; ive 4; Mismatches 24; Indels
                                                                                                                                                                          33; Indels
Balaban N.;
Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; L41654; AAA65193.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Grueter E., Betschart B.;

Grueter E., Betschart B.;

Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ287609; CAB76184.1; -.

EMBL; AJ287599; CAB76183.1; -.

EMBL; AJ287599; CAB76181.1; -.

EMBL; AJ287599; CAB76181.1; -.

GO; GO:000786; C:nucleosome; IEA.

GO; GO:0005677; F:DNA binding; IEA.

GO; GO:0005334; P:nucleosome assembly; IEA.
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                                                                                    C2AFF4265101BBBC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                               DB 2;
                                                                                                                          Score 97.5; DB; Pred. No. 4; 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               76 AA
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                                                                                                                                                                                                                                                                                                                                                  58 KKVAPKKVVAKKVAPKKVAGKKAAAKKA 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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Name=H1D76; Synonyms=H1A76, H1C76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR005819; Histone_H5.
PRINTS; PR00624; HISTONEH5.
                                                                                                                            23.8%;
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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June Run on:

3, 2005, 11:16:19 ; Search time 157 Seconds
 (without alignments)
211.856 Million cell updates/sec

US-10-792-311-6 409 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 segs, 386760381 residues Searched:

1117955 Total number of hits satisfying chosen parameters:

length: 0 length: 86 Bed Bed 88 Minimum

Maximum

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

A_Geneseq_16Dec04:* •• Database

geneseqp1980s:* geneseqp1990s:*

geneseqp2003as:* geneseqp2003bs:* geneseqp2001s:* geneseqp20028:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

## SUMMARIES

Description	Aay82576	Aay82575 Copolymer	-		Abg71044 Tumour ne	_	_	Adk15632 Nucleatin	Adel0612 Structura	Adk15631 Nucleatin	Abg71043 Tumour ne	Adel0608 Structura	Adk15627 Nucleatin		Adk15681 Library f		Adk15664 Nucleatin	Adel0658 Structura	Adk15677 Library f	Adel0605 Structura	Adk15624 Nucleatin	Adel0610 Structura	Adk15629 Nucleatin	Adel0606 Structura	Adk15625 Nucleatin
ID	AAY82576	AAY82575	AAY82574	AAY82573	ABG71044	AAY82572	ADE10613	ADK15632	ADE10612	ADK15631	ABG71043	ADE10608	ADK15627	ADE10662	ADK15681	ADE10645	ADK15664	ADE10658	ADK15677	ADE10605	ADK15624	ADE10610	ADK15629	ADE10606	ADK15625
DB	6	m	٣	m	Ŋ	٣	7	œ	7	æ	'n	7	æ	7	œ	7	80	7	œ	7	œ	۲	œ	7	8
% Query Match Length	98	77	99	99	80	45	79	79	86	86	9	85	85	98	98	83	83	85	85	83	83	79	79	80	80
* Query Match	100.0	85.9	65.5	57.0	33.9	6.08	28.2	28.2	28.2	28.2	28.1	27.8	27.8	27.5	27.5	27.3	27.3	27.0	27.0	26.8	26.8	26.5	26.5	26.5	26.5
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Score		351.5	268	233	138.5	126.5	115.5	115.5	115.5	115.5	115	113.5	113.5	112.5	112.5	111.5	111.5	110.5	110.5	109.5	109.5	108.5	108.5	108.5	108.5
Result No.	П	7	ю	4	'n	y	7	00	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Adel0611 Structura Adk15630 Nucleatin Aay82571 Copolymer Adel0660 Structura Adel0660 Structura				Ads15345 Yeast zuo Ade10655 Structura Adk15674 1.ibrary f Aar28871 High affi Ade10654 Structura
ADE10611 ADK15630 AAY82571 ADE10660	ADK15679 ADE10695 ADK15714	ADK15680 ADE10604 ADK15623	ADE10646 ADK15665 AAW24449 ADO04487	ADS15345 ADE10655 ADK15674 AAR28871 ADE10654
85 7 35 3	83 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7	85 78 78 78 8		60 8 83 7 83 8 46 2 78 7
2 2 2 2 2 2 2 2 2 2 2 3 2 3 2 3 3 3 3 3	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	25.6 25.6 25.6	22 22 22 22 22 22 22 22 23 23 23 23 23 2	24.8 24.4 24.4 24.8 3.3 4.3 3.3
108.5 108.5 108	105.5	105.5 104.5 104.5	102 102 101.5 101.5	101.5 101.5 101.5 100
25 28 28 28	0 1 2 2	3 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	33 38 40 40	14444 1444 1454 1544 1544 1544 1544 154

## ALIGNMENTS

Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyrodi; antiinflammatory; antidabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; peoriasis; pemphigus vulgaris; systemic lupus erythematosus. Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:6. AAY82576 standard; peptide; 86 AA. (first entry) 28-JUL-2000 RESULT 1 AAY82576 

Unidentified

WO200018794-A1.

06-APR-2000.

99WO-US022402. 24-SEP-1999; 98US-0101693P. 25-SEP-1998; (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.

Gad A, Lis D;

WPI; 2000-317499/27.

Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.

Claim 10; Page 14; 72pp; English.

AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides

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cetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune thyroiditis, autoimmune thyroiditis, autoimmune thyroiditis, autoimmune thyroiditis, autoimmune backers, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myrosdema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated mediated diseases which can be treated include host-versus-graft disease, colypeptides of the invention have defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as molecular weight markers
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the invention are used as molecular weight markers for glatiramer
                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 409; DB 3; Length 86;
; Pred. No. 7e-30;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 YKAEAAKKAYKAEAAKAAAKEAAYEA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 YKAEAAKKAYKAEAAKAAAKEAAYEA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY82575 standard; peptide; 77 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
100.0%;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 86 AA;
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weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer acetate related terrapolymers. The polypeptides may also be used for treating and preventing immune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating the polyperiors.
                                                                                                                                                                                                                                                                                       diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune opportitis, sutcoimmune thyroiditis, autoimmune thyroiditis, autoimmune thyroiditis, autoimmune uveoretinitis, Crohn's disease, chronic immune thrombocytopaenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated mediated diseases which can be treated include host-versus-graft disease, polypeptides of the invention have defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as molecular weight markers
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89.5%; Pred. No. 9.9e-25;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY82574 standard; peptide; 66 AA.
                       Claim 10; Page 14; 72pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US022402.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 89.5<sup>3</sup>
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 77 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200018794-A1.
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(YEDA ) YEDA RES & DEV CO LTD.

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Weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight TV-marker polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer acetate related tetraplymers. The polypeptides may also be used for aseases. Such diseases include either cell-mediated or antibody-mediated diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune thyroiditis, autoimmune uveoretinitis, contact sensitivity disease, diabetes mellitus, Graves disease, Chronic immune thrombocytopaenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, psoriaais, pemphigus vulgaris, or systemic lupus erythematosus. Mediated mediated diseases which can be treated include host-versus-graft disease, and delayed-type hypersensitivity. The polypeptides of the innext of a treated include host-versus-graft disease proposed the proposed proposed to the innext of the proposed proposed proposed to the proposed proposed proposed proposed proposed to the proposed prop
                                                                                                                                                                                                                         Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.
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                                                                                                                                                                                                                                                                                                                                            Claim 10; Page 14; 72pp; English.
(TEVA-) TEVA PHARM USA INC
                                                                                                                                              API; 2000-317499/27
                                                                           Gad A,
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Sequence 66 AA;

1 AKKYAKKEKAYAK-----AKKAEAK------AAKKAKAEAKKYAKAKAEKEKYAKAYAEAKA 49 1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAKAEAKKYAKAAKAEKKEYAAAEAK 1; Indels 20; Gaps 65.5%; Score 268; DB 3; Length 66; 75.6%; Pred. No. 3e-17; ive 0; Mismatches 1; Indels 61 YKAEAAKKAYKAEAAKAAAKEAAYEA 86 -----YKAEAAKAAAKEAAYEA 66 Query Match Best Local Similarity 75.69 ઠ a ò g

'n 9

RESULT 4

AAY82573 standard; peptide; 56 AA. AAY82573; AAY.82573 

Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:3.

28-JUL-2000 (first entry)

Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidabetic; thyromimetic; haemostetic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; theumatoid arthritis; crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.

Jnidentified

WO200018794-A1

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AMYREA'L TO AMYREA'LY TEPERSENT SPECIFICALLY CLAIMED CODOLYMET MOLECULAR WEIGHT TWO AMYREA'LY COMPARED FOR THE PRESENT INVENTION GENERALLY CLAIMED AS AN INCIDENTIFIED MOLECULAR WEIGHT AND AND CAT A CORDINGER (EP) WHICH has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer of the invention are used as molecular weight markers for glatiramer of the invention are used as molecular weight markers for glatiramer of the invention are used as molecular weight markers for glatiramer of the invention are used for a mammal. Autoimmune diseases which may be treated include atthritic conditions, demyelinating diseases include arthritic conditions, demyelinating arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune arthritis, autoimmune thrombocytopaenia purpura, colitis, contact cophoritis, autoimmune thrombocytopaenia purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Grillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, sporiated diseases which can be treated include host-versus-graft disease, and delayed-type hypersensitivity. The graft-versus-host disease, and delayed-type hypersensitivity. The copypeptides of the invention have defined molecular weights and physical properties which are analogous to glatiramer accetate molecules, which makes them ideal for use as molecular weight markers
                                                                                                                                                                                                                                                                                                                                                                                                                            AAY82571 to AAY82577 represent specifically claimed copolymer molecular
                                                                                                                                                                                                                                                                                                              Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.
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                                                                                                                                                                                                                                                                                                                                                                                  Claim 10; Page 14; 72pp; English
                                                                 99WO-US022402.
                                                                                                           98US-0101693P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                 WPI; 2000-317499/27
                                                                                                                                                   (YEDA ) YEDA RES & (TEVA-) TEVA PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 56 AA;
                                                                                                                                                                                                                         3ad A, Lis D;
                                                                 24-SEP-1999;
                                                                                                           35-SEP-1998;
                       06-APR-2000
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                                                                                                                                                                             (TEVA-)
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8
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1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAK 60 30; -----YKAEAAKAAAKEAYEA 56

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ABG71044 standard; peptide; 80 AA. (first entry) 16-DEC-2002 ABG71044; ABG71044 RESULT 

Tumour neoangiogenesis associated peptidase substrate peptide #8

Tumour necanglogenesis; peptidase substrate; tumour related disorder; tumour-selective intravascular coagulation inducing molecule; blood clotting; tumour vascularisation; tumour growth control; heparin-binding peptide.

Synthetic.

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New tumor-selective intravascular coagulation inducing molecules useful
                             17. 24
/note= "Optionally absent"
25. 32
/note= "Optionally absent"
                    "Optionally absent"
                                                        33. .40
/note= "Optionally absent"
                                                                     49. .56
/note= "Optionally absent"
                                                                                                    .64
.e= "Optionally absent"
                                                                                                                                           /note= "Optionally absent"
                                                                                                                 ...72
...72
^+e= "Optionally &
       Location/Qualifiers
                                                                                                                                                                                                                                                                                      Claim 20; Page 27; 40pp; English.
                                                                                                                                                                                                                   (UYLO-) UNIV CATHOLIQUE LOUVAIN
                                                                                                                                                                                       30-JAN-2002; 2002WO-EP000951
                                                                                                                                                                                                     30-JAN-2001; 2001EP-00870017
                                                                                                                                                                                                                                                                      for control of tumor growth
               ). .16
/note=
                                                                                                             'note=
                                                                                /note=
                                                                                                                             /note=
                                                                                                                                                                                                                                   Dubois V;
                                                                                                                                                                                                                                                WPI; 2002-706887/76.
                                                          Misc-difference 33
                                                                                       Misc-difference 49
                            Misc-difference 17
              Misc-difference 9.
                                           Misc-difference
                                                                                                                                   Misc-difference
                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                              Sequence 80 AA;
                                                                                                                                                         WO200260488-A1
                                                                                                                                                                                                                                   Trouet A,
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invention describes tumour-selective intravascular coagulation

inducing molecules. The molecules are useful as a medicine and in the manufacture of a medicament for the treatment and/or prevention of tumour related disorders. The compounds are able to induce blood clotting at tumour sites resulting in the disruption of the tumour vascularisation and consequently in the control of tumour growth. This sequence represents a heparin-binding peptide, a postively charged polymer that can be incorporated into a substrate for extracellular hydrolases releasable by tumour or neoangiogenic endothelial cells

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65
                                                                           6 KKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEA
                             11; Gaps
 Length 80;
                             19; Indels
33.9%; Score 138.5; DB 5;
53.7%; Pred. No. 1.9e-05;
iive 8; Mismatches 19;
                              Conservative
Query Match
Best Local Similarity
Matches 44; Conserv
                             44;
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66 A-KKAYKA---EAAKAAKEAA 83 | ||| || :|| serkaarkkaa 78

AAY82572 standard; peptide; 45 AA. AAY82572; RESULT 6 AAY82572

28-JUL-2000 (first entry) axxxex

AXY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides [1] for determining the molecular weight invention describes polypeptides [1] for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatizamer actatate and preventing immune diseases may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases of treated include either cell-mediated or antibody-mediated diseases such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatory complexitis, autoimmune thyroiditis, e.g. multiple sclerosis, contact cophoritis, autoimmune thyroiditis, autoimmune vivocretinitis, contact cophoritis, autoimmune thyroiditis, autoimmune baseolytic anaemia, autoimmune cophoritis, autoimmune thyroiditis, autoimmune servicimune thyroiditis, autoimmune servicimune thyroiditis, disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myaethenia gravis, contact sensitivity disease, disease, idiopathic myxoedema, myaethenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated mediated diseases which can be treated include host-versus-graft disease, cromostides which are analogous to glatizamer acetate molecules, which are analogous to glatizamer acetate molecules, which m • Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus. 1 AKKYAKEKAYAKKAEKAAKKAEAKYYAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAK 60 Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:2. 41; 30.9%; Score 126.5; DB 3; Length 45; 45.3%; Pred. No. 0.00013; ive 0; Mismatches 6; Indels 4: Claim 10; Page 14; 72pp; English. CO LTD. 99WO-US022402 98US-0101693P 39; Conservative (YEDA ) YEDA RES & DEV (TEVA-) TEVA PHARM USA Best Local Similarity WPI; 2000-317499/27 Sequence 45 AA; WO200018794-A1 Gad A, Lis D; 24-SEP-1999; 35-SEP-1998; Unidentified Query Match Matches ð

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., .,

Gaps

28.2%; Score 115.5; DB 7; Length 79; 44.2%; Pred. No. 0.0023; ive 16; Mismatches 14; Indels 13;

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Example 6; SEQ ID NO 20; 110pp; English
   ADE10613 standard; protein; 79 AA.
                                                                                       20-JUN-2002; 2002US-00177725
                                                                                              98US-00169015
                                                                                                 99US-00415765
                  (first entry)
                                                                                                                Peelle BR,
                                                                                                         (RIGE-) RIGEL PHARM INC
                                                                                                                       WPI; 2003-829786/77.
                                                                        US2003143562-A1
                                                                                              08-OCT-1998;
                                                                                                 08-OCT-1999;
                 29-JAN-2004
                                                                                                                Anderson D,
                                                                               31-JUL-2003
                                                                 Synthetic.
                                                                                                                                                                                                                                                cell-cell
          ADE10613;
                                                                                                                                          nethods
ADE10613
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its quantity. The expression of structurally biased libraries generate elevated cellular concentration of peptides having a given structural bias and thus increase the hit rate for targets that bind such structures. This is the amino acid sequence of a protein associated with fused nucleic acid and random peptide libraries of the invention.
can easily be monitored, both for its presence within cells and
                                                                                                                                                                                                                                                                                                                             Local Similarity 44.2
nes 34; Conservative
                                                                                                                                                                                                                              Sequence 79 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADK15632;
                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sednence
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                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention describes a library (I) of fusion nucleic acids, where each fusion nucleic acid comprises a first nucleic acid (NI), encoding a caffold protein sequence; and a second nucleic acid (NI), encoding a library peptide sequence; and a second nucleic acid (NI), encoding a library peptide sequence; and a second nucleic acid (NI), encoding a library peptide sequence; and second nucleic acid (NI), encoding a classification of sequence; where NI is fused to N2. Disclosed is a method for screening bioactive peptides conferring a change in specific phenotype such as cell morphology, cell growth, cell viability, adhesion to substrates or other cells, and cellular density; changes in the expression of one or more RNAs, proteins, lipids, hormones, cytokines, or other molecules; ctc. The bioactive peptide identified by above mentioned method is used to generate more candidate peptides and to identify target molecules; etc. The bioactive peptide interacts. The peptide(s) can be combined with other pharmacologic activators to study the epistatic colling also useful in cancer applications. Random libraries can be cintroduced into any tumour cell (primary or cultured), and peptides cintroduced into any tumour cell (primary or cultured), and peptides division or decreased cell growth. The method is also useful for corresponded cell growth. The method is also useful for corresponded cell growth. The method is also useful for introduced into any tumour cell (primary or cultured), and peptides which by themselves induce apoptosis, cell death, loss of cell division or decreased cell growth. The method is also useful for corresponded cell growth. The method is also useful for introduced into any tumour suppressor genes coll important in hereat cancer such as the adenomateus polyposis coll gene cell important in hereat cancer such as the adenomateus polyposis coll gene cell important in hereat cancer such as the adenomateus polyposis coll genes in a more cell prince of the processor genes and coll cell cell cell cell cell ce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel library of fusion nucleic acids each of which has fused first and second nucleic acids encoding scaffold protein and library peptide having alpha helical biasing sequence, respectively, useful in screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (APC) and the Drosophila discs-large gene (DIg), which are components of cell-cell junctions. The methods are useful in cardiovascular applications, neurobiology applications, bone biology applications, skin
                                                                                                                                                                                                                                                                                                                      fusion nucleic acid library; scaffold protein; bioactive peptide; phenotype change; cell morphology; cell growth; cell viability; cell adhesion; cellular density; cancer; tumour; apoptosis; cell death; loss of cell division; decreased cell growth; brca-1; brca-2; tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC; brosophila discs-large; DIG; cardiovascular; neurobiology; bone biology; skin biology; cosmeceutical; endocrinology; infectious disease; drug toxicity; drug resistance; inflammation; allergic response.
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                                                                                                                                                                                                                                                                Structurally biased random peptide library related protein segid 20.
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The invention comprises a library of fusion nucleic acids, where each encoded protein contains a scaffold protein (e.g. a green fluorescent protein - GFP) and a library peptide sequence comprising an alpha helical biasing sequence, or a scaffold protein, a library peptide and a nucleating sequence. The library of the invention is useful for screening bloactive peptides conferring a particular phenotype. The present amino acid sequence represents a library protein containing a nucleating
   69
                                                                     Library of fusion polypeptides in which each polypeptides comprises scaffold protein and library peptide having alpha helical biasing sequence, or scaffold protein, library peptide and nucleating sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fusion nucleic acid library; fusion protein library; scaffold protein; green fluorescent protein; GFP; alpha helical biasing sequence; nucleating sequence; screening.
18 AAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKK-----EYAAAEAKYKAEAAKKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleating sequence-containing library fusion protein #14.
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                                                                                                                                                                                                                                                                                                                                                                                                                    ADK15632 standard; peptide; 79
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08-OCT-1999; 99US-00415765.
20-JUN-2002; 2002US-00177725.
                                                                                                                                                   70 YKAEA----AKAAKEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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The invention describes a library (I) of fusion nucleic acids, where each fusion nucleic acid comprises a first nucleic acid (NI), encoding a caffold protein sequence; and a second nucleic acid (N2), encoding a library peptide sequence comprising an alpha helical biasing sequence; where NI is fused to N2. Disclosed is a method for screening bloactive peptides conferring a change in specific phenotype such as cell compromed. Compared to N2. Disclosed is a method for screening bloactive peptides conferring a change in specific phenotype such as cell compared to N2. Disclosed is a method for screening bloactive. Cells, and cells, and cells, changes in the expression of one or more RNAs, proteins, lipids, hormones, cytokines, or other molecules; changes in the equilibrium state (i.e., half-life) or one or more RNAs, protein, lipids, hormones, cytokines, or other molecules; etc. The bioactive peptide identified by above mentioned method is used to generate more candidate peptides and to identify target molecules, i.e., the molecules with which the bioactive peptide interacts. The peptide(s) can be combined with other pharmacologic activators to study the epistatic combined with other pharmacologic activators to study the epistatic combined with other pharmacologic activators to study the epistatic combined with other pharmacologic activators to study the epistatic combined with other pharmacologic activators to study the epistatic combined with other pharmacologic activators to study the epistatic combined with other pharmacologic activators to study the epistatic combined method is also useful in cancer applications. Random libraries can be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fusion nucleic acid library; scaffold protein; bioactive peptide; phenotype change; cell morphology; cell growth; cell viability; cell adhesion; cellular density; cancer; tumour; apoptosis; cell death; loss of cell division; decreased cell growth; brca-1; brca-2; tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC; brosophila disca-large, blg; cardiovascular; neurobiology; bone biology; skin biology; cosmeceutical; endocrinology; infectious disease; drug toxicity; drug resistance; inflammation; allergic response.
                                                                                                 69
                                                                                                                             Novel library of fusion nucleic acids each of which has fused first and
                                                                                                 18 AAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKK------EYAAAEAKYKAEAAKKA
                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Structurally biased random peptide library related protein seqid 19.
                                                  13;
  Length 79;
                                                  Indels
28.2%; Score 115.5; DB 8; 44.2%; Pred. No. 0.0023; ive 16; Mismatches 14;
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                                                                                                                                                                                                                                                                                                                                                                ADE10612 standard; protein; 86 AA
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                                                                                                                                                                                                                                           60 KEAEAKAKEAEAKAKEA 76
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99US-00415765
                                                                                                                                                                                              70 YKAEA----AKAAKEA
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                                             34; Conservative
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                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                ADE10612;
Query Match
Best Local 8
                                                  Matches
                                                                                                                                                                                                                                                                                                                 RESULT 9
ADE10612
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introduced into any tumour cell (primary or cultured), and peptides identified which by themselves induce apoptosis, cell death, loss of cell division or decreased cell growth. The method is also useful for screening of bioactive peptides which restore the constitutive function of the brca-1 or brca-2 genes, and other tumour suppressor genes
                                                                              of the broad or broad genes, and other tumour suppressor genes important in breast cancer such as the adenomatous polyposis coli gene (ARC) and the brosophila discs-large gene (Dig), which are components of cell-cell junctions. The methods are useful in cardiovascular applications, neurobiology applications, bone biology applications, skin applications, infectious disease applications, drug toxicities and drug resistance applications immunobiology, inflammation, and allergic response applications, and biotechnology applications. The peptide library can easily be monitored, both for its presence within cells and its quantity. The expression of structurally biased libraries generate elevated cellular concentration of peptides having a given structural bias and thus increase the hit rate for targets that bind such bias and thus increase the hit rate for targets that bind such bias and thus increase the hit rate for targets that bind such bias and thus increase the hit rate for targets that bind such bias and thus how the concentration of the periods are provedured.
                                                                                                                                                                                                                                                                                                                                                                  structures. This is the amino acid sequence of a protein associated with fused nucleic acid and random peptide libraries of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 KEKAYAKKAEKAAKKAEAKA----YKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAKYK 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fusion nucleic acid library; fusion protein library; scaffold protein; green fluorescent protein; GFP; alpha helical biasing sequence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 115.5; DB 7; Lucar
Pred. No. 0.0025;
Transches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADK15631 standard; peptide; 86 AA.
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08-OCT-1999; 99US-00415765.
20-JUN-2002; 2002US-00177725.
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Best Local Similarity 39.0%
Loca 33; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 86 AA;
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ADK15631
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Dubois V;

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Trouet A,
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                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                              RESULT 12
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               The invention comprises a library of fusion nucleic acids, where each encoded protein contains a scaffold protein (e.g. a green fluorescent protein - GFP) and a library peptide sequence comprising an alpha helical biasing sequence, or a scaffold protein, a library peptide and a nucleating sequence. The library of the invention is useful for screening bioactive peptides conferring a particular phenotype. The present amino acid sequence represents a library protein containing a nucleating
                                                                                                                                                              62
                                                                                                                                                                                9
                                                                                                                                                              7 KEKAYAKKAEKAAKKAEAKA----YKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAKYK
                                                                                                                                                                                Tumour necanglogenesis; peptidase substrate; tumour related disorder; tumour-selective intravascular coagulation inducing molecule; blood clotting; tumour vascularisation; tumour growth control; heparin-binding peptide.
                                                                                                                                                                                                                                                                                                                              Tumour neoangiogenesis associated peptidase substrate peptide #7.
                                                                                                                                           7;
                                                                                                                         Length 86;
                                                                                                                                           Indels
                                                                                                                       28.2%; Score 115.5; DB 8; 39.8%; Pred. No. 0.0025; iive 18; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference 19. .24
/note= "Optionally absent"
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//note= "Optionally absent"
Misc-difference 55. .60
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/note= "Optionally absent"
Misc-difference 43. .48
/note= "Optionally absent"
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/note= "Optionally absent"
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 6; SEQ ID NO 19; 110pp; English.
                                                                                                                                                                                                    82
                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                      ABG71043 standard; peptide; 60 AA.
                                                                                                                                                                                                    63 AEAAKKAYKAEA---AKAAAKEA
                                                                                                                                                                                                                      AKAAEAEAKAKAEAEAKAKAAEA
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                                                                                                                               Local Similarity 39.8%
les 33; Conservative
                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference 25
                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                     Sequence 86 AA;
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                                                                                                                                                                                                                                                                                                           16-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
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                                                                                                                        Query Match
                                                                                                                                 Best Loc
Matches
                                                                                                                                                                                                                                                   RESULT 11
8X22222228
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Novel library of fusion nucleic acids each of which has fused first and second nucleic acids encoding scaffold protein and library peptide having alpha helical biasing sequence, respectively, useful in screening
                                                                                                                                                                                                                                                                                                                         tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fusion nucleic acid library; scaffold protein; bioactive peptide; phenotype change; cell morphology; cell growth; cell viability; cell adhesion; cellular density; cancer; tumour; apoptosis; cell death; loss of cell division; decreased cell growth; brca-1; brca-2; tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC; bosoophila discs-large, blg; candiovascular; neurobiology; bone biology; skin biology; cosmeceutical; endocrinology; infectious disease; drug toxicity; drug resistance; inflammation; allergic response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AKKA-RAAKK--ARAAKKARAAKKARA----AKKARAAKK----ARAAKKARAAKKARA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 AKKAEKAAKKAEAKAYKAABAKKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEAAKKAYK 71
                                                                   tumor-selective intravascular coagulation inducing molecules useful
                                                                                                                                                                                                                                                                            inducing molecules. The molecules are useful as a medicine and in the manufacture of a medicament for the treatment and/or prevention of tumo related disorders. The compounds are able to induce blood clotting at tumour sites resulting in the disruption of the tumour vascularisation and consequently in the control of tumour growth. This sequence represents a heparin-binding peptide, a postively charged polymer that can be incorporated into a substrate for extracellular hydrolases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Structurally biased random peptide library related protein seqid 15.
                                                                                                                                                                                                                                              invention describes tumour-selective intravascular coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          releasable by tumour or neoangiogenic endothelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 115; DB 5;
Pred. No. 0.0019;
6; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bogenberger JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADE10608 standard; protein; 85 AA.
                                                                                                                                                                           Claim 20; Page 27; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28.1%;
52.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-00169015
99US-00415765
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                                                                                                        for control of tumor growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 AKKARAAKKARA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peelle BR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (RIGE-) RIGEL PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 AEAAKAAAKEAA
WPI; 2002-706887/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TPI; 2003-829786/77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JS2003143562-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 60 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-OCT-1998;
08-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-JUL-2003
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Fri

18-MAR-2003; 2003US-00393449

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                                                                          C fusion nucleic acid comparises a first nucleic acid (N1), encoding a caffeld protein sequence; and a second nucleic acid (N2), encoding a caffeld protein sequence; and a second nucleic acid (N2), encoding a library peptide sequence; and a second nucleic acid (N2), encoding a library peptide sequence; and a second nucleic acid (N2), encoding a library peptide sequence comprising a change in specific phenotype such as cell encyphology, cell growth, cell viability, adhesion to substrates or other morphology, cell growth, cell viability, adhesion to substrates or other morphology, cell growth, cell viability, adhesion to substrates or other morphology, cell growth, cell viability, adhesion to substrates or other molecules; in the equilibrium state (i.e., half-life) or one or more RNAs, protein, cells, and cellular density; changes in the expression of one or more RNAs, proteins, lipids, hormones, cytokines, or other molecules; i.e., the molecules in the equilibrium state (i.e., half-life) or one or more RNAs, protein, cell identified by above mentioned method is used to generate more peptide interacts. The peptide (s) can be with which the bioactive peptide interacts. The peptide(s) can be candidate peptides and to identified which by themselves induce apoptications. Random libraries can be method is also useful in cancer applications, Random libraries can be introduced into any tumour cell (primary or cultured), and peptides method is also useful for division or decreased cell growth. The method is also useful for division or decreased cell growth. The method is also useful for compensing of bioactive peptides which restore the components of the broa-1 or broa-2 genes, and other tumour suppressor genes (RNC) and the brosophila discalars, and other tumour suppressor genes (ARC) and the brosophila discalars, and other tumour suppressor gene (RNC) and the brosophila discalars, manuology applications, and brocenhology applications, and brocenhology applications, and brocenhology applications, and brocenhology applic
                                                                   The invention describes a library (I) of fusion nucleic acids, where each
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fusion nucleic acid library; fusion protein library; scaffold protein; green fluorescent protein; GFP; alpha helical biasing sequence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 AAKKAEAKAYKAAEAKKKAK------AEAKKYAKAKAEKKEYAAEAKYKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 7; Length 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleating sequence-containing library fusion protein #9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27.8%; Score 113.5; DB 7;
41.0%; Pred. No. 0.0038;
tive 14; Mismatches 20;
                                Example 6; SEQ ID NO 15; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADK15627 standard; peptide; 85 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 EAAKKAYKAEAAKAAAKEAAYEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleating sequence; screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 41.0%
les 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 85 AA;
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methods
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Matches
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US2003224412-A1

Synthetic.

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The invention comprises a library of fusion nucleic acids, where each encoded protein contains a scaffold protein (e.g. a green fluorescent protein - GFP) and a library peptide sequence comprising an alpha helical biasing sequence, or a scaffold protein, a library peptide and a nucleating sequence. The library of the invention is useful for screening bioactive peptides conferring a particular phenotype. The present amino acid sequence represents a library protein containing a nucleating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fusion nucleic acid library; scaffold protein; bioactive peptide; phenotype change; cell morphology; cell growth; cell viability; cell adhesion; cellular density; cancer; tumour; apoptosis; cell death; loss of cell division; decreased cell growth; brca-1; brca-2; tumour suppressor gene; breast cancer; adenomatous polyposis coli; APC; brosophila discs-large, DIg; cardiovascular; neurobiology; bone biology; skin biology; cosmeceutical; endocrinology; infectious disease; drug toxicity; drug resistance; inflammation; allergic response;
                                                                                                                                                                                                                                                                                                 Library of fusion polypeptides in which each polypeptides comprises scaffold protein and library peptide having alpha helical biasing sequence, or scaffold protein, library peptide and nucleating sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Structurally biased random peptide library scaffold protein seqid 69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27.8%; Score 113.5; DB 8; Length 85; 41.0%; Pred. No. 0.0038; ive 14; Mismatches 20; Indels 1
                                                                                                                                                                                                    Bogenberger JM
                                                                                                                                                                                                                                                                                                                                                                                                     Example 6; SEQ ID NO 15; 110pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 EAAKKAYKAEAAKAAAKEAAYEA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADE10662 standard; protein; 86 AA.
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60 kaaeaeakakaaeaeakakaaea
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08-OCT-1998; 98US-00169015.
08-OCT-1999; 99US-00415765.
20-JUN-2002; 2002US-00177725.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34; Conservative
                                                                                                                                                        BOGENBERGER J M.
                                                                                                                                                                                                 Anderson D, Peelle BR,
                                                                                                                                                                                                                                                     WPI; 2004-033956/03.
                                                                                                  (ANDE/) ANDERSON D.
(PEEL/) PEELLE B R.
(BOGE/) BOGENBERGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 85 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence
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the invention describes a library (1) of tusion nucleic acid.

the invention describes a library (1) of tusion nucleic acid (N2), encoding a scaffold protein sequence; and a second nucleic acid (N2), encoding a clibrary peptide sequence comprising an alpha helical biasing sequence; where NI is fused to N2. Disclosed is a method for screening bicactive peptides conferring a change in specific phenotype such as cell controlled to the sequence; peptides conferring a change in specific phenotype such as cell controlled to the sequence of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  structures. This is the amino acid sequence of a scaffold protein used in peptide libraries ot hold the library peptide in a conformationally
                                                                                                                                                                                                                                                                                                 Novel library of fusion nucleic acids each of which has fused first and second nucleic acids encoding scaffold protein and library peptide having alpha helical biasing sequence, respectively, useful in screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention describes a library (I) of fusion nucleic acids, where each
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          response applications, and biotechnology applications. The peptide
library can easily be monitored, both for its presence within cells and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              its quantity. The expression of structurally biased libraries generate elevated cellular concentration of peptides having a given structural bias and thus increase the hit rate for targets that bind such
                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 69; 110pp; English
                                                                                                                                                                                               Bogenberger JM;
20-JUN-2002; 2002US-00177725.
                                                                                 99US-00415765
                                                                                                                                                                                               Peelle BR,
                                                                                                                                        (RIGE-) RIGEL PHARM INC
                                                                                                                                                                                                                                                WPI; 2003-829786/77.
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                                                         08-OCT-1998;
                                                                                   08-OCT-1999;
                                                                                                                                                                                               Anderson D,
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                                                           ----YKAAEAKKKAKAEA 40
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                                                                          29; Gaps
           27.5%; Score 112.5; DB 7; Length 86; 42.0%; Pred. No. 0.0047; Live 6; Mismatches 16; Indels 25
                                                            7 KEKAYAKKAEKAAKKAEAKA----
                                    Conservative
Query Match
Best Local Similarity
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The invention comprises a library of fusion nucleic acids, where each encoded protein (e.g. a green fluorescent protein contains a scaffold protein (e.g. a green fluorescent protein - GFP) and a library peptide sequence comprising an alpha helical biasing sequence, or a scaffold protein, a library peptide and a nucleating sequence. The library of the invention is useful for screening bioactive peptides conferring a particular phenotype. The present amino acid sequence represents a scaffold protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----YKAAEAKKKAKAEA 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Library of fusion polypeptides in which each polypeptides comprises scaffold protein and library peptide having alpha helical biasing sequence, or scaffold protein, library peptide and nucleating sequence.
                                                                                                            fusion nucleic acid library; fusion protein library; scaffold protein; green fluorescent protein; GFP; alpha helical biasing sequence; nucleating sequence; screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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42.0%; Pred. No. 0.0047;
ive 6; Mismatches 16; Indels
                                                                                      Library fusion protein-related scaffold protein #13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 69; 110pp; English
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ADK15681 standard; peptide; 86 AA.
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08-OCT-1999; 99US-00415765.
20-JUN-2002; 2002US-00177725.
                                                                                                                                                                                                                                                                 18-MAR-2003; 2003US-00393449
                                                           (first entry
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                                                                                                                                                                                                                                                                                                                                                                                                                  Peelle BR,
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                                                                                                                                                                                                         JS2003224412-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 86 AA;
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                                                           36-MAY-2004
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                                                                                                                                                                                                                                      04-DEC-2003.
                                                                                                                                                                          Synthetic.
                                ADK15681;
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(BOGE/)
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3, 2005, 11:34:20 ; Search time 136 Seconds (without alignments) 218.592 Million cell updates/sec
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1: \( cgn2 \frac{6}\) \text{prodata} \( 1\) \text{PubCoMB.pep:*} \\
2: \( cgn2 \frac{6}\) \text{prodata} \( 1\) \text{PubCoMB.pep:*} \\
2: \( cgn2 \frac{6}\) \text{prodata} \( 1\) \text{PubDa} \( 1\) \text{PuBCOMB.pep:*} \\
4: \( cgn2 \frac{6}\) \text{prodata} \( 1\) \text{PubDa} \( 1\) \text{PuBCOMB.pep:*} \\
5: \( cgn2 \frac{6}\) \text{prodata} \( 1\) \text{PubDa} \( 1\) \text{PuBCOMB.pep:*} \\
5: \( cgn2 \frac{6}\) \text{prodata} \( 1\) \text{PubDa} \( 1\) \text{PuBCOMB.pep:*} \\
7: \( cgn2 \frac{6}\) \text{prodata} \( 1\) \text{PubDa} \( 1\) \text{PuBCOMB.pep:*} \\
7: \( cgn2 \frac{6}\) \text{prodata} \( 1\) \text{PubDa} \( 1\) \text{PuBCOMB.pep:*} \\
9: \( cgn2 \frac{6}\) \text{prodata} \( 1\) \text{PubDa} \( 1\) \text{PuBCOMB.pep:*} \\
10: \( cgn2 \frac{6}\) \text{prodata} \( 1\) \text{PubDa} \( 1\) 
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                            OM protein - protein search, using sw model
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409
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                                                                                                                                                                                                                                                                                                                     June
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Searched:
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                                                                                                                                                                                                                                                                                                                     Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Description	Sequence 6, Appli	Sequence 6, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 20, Appl	Sequence 20, Appl	
ΙD	US-09-816-989A-6	US-10-792-311-6	US-09-816-989A-5	US-10-792-311-5	US-09-816-989A-4	US-10-792-311-4	US-09-816-989A-3	US-10-792-311-3	US-09-816-989A-2	US-10-792-311-2	US-10-177-725-20	US-10-393-449-20	US-10-177-725-19
DB	6	17	σ	17	0	17	6	17	σ	17	14	15	14
* Query Match Length DB	98	98	77	77	99	99	26	99	45	45	79	79	98
Query Match	100.0	100.0	85.9	85.9	65.5	65.5	57.0	57.0	30.9	30.9	28.2	28.5	28.2
Score	409	409	351.5	351.5	268	268	233	233	126.5	126.5	115.5	115.5	115.5
Result No.	-	7	e	4	ß	9	7	ω	6	10	11	12	13

10 3000	2	Sequence 15, Appl		Sequence 69, Appl				52,	65,	65,	20,	12,	12,	17,	Sequence 17, Appl	H	H	ä	Sequence 18, Appl	ä	Sequence 1, Appli	67,	67,	102			68,	11,	Н	53,	23,	16,
01 077 606 01 011				US-10-177-725-69		703		US-10-393-449-52	US-10-177-725-65	US-10-393-449-65	0	12	7	US-10-177-725-17	1.1	US-10-177-725-13	3		US-10-393-449-18	S		0-177-725-67		0-177-725-102	0-393-449-102	0-177-725-68	0-393-449-68	0-177-725-11	-449-11	0-177-725-53	0-393-449-53	US-10-390-472-16
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•	14	15	16	17	18	19	50	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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US-09-816-989A-6
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                                                                                                                                                                                                                            Length 86;
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                                                                                                                                                                                                                           / Match
Local Similarity 100.0%; Pred. No. 3.5e-28; Nes 86; Conservative 0; Mismatches 0;
                                                                                                                                                                                   ORGANISM: Artificial Sequence
RESULT 1
US-09-816-989A-6
                                                                                                                                                                   LENGTH: 86
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Matches
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61 YKABAKKAYKABARAAKBAAYBA 86

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APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKE
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKE
FILLS OF INVENTION: AND FOR THERAPEUTIC USE
FILLS REPRENCE: 2609/60807-4-PCT-US
CURRENT APPLICATION NUMBER: US/10/792,311
CURRENT APPLICATION NUMBER: US/10/792,311
PRIOR FILLNG DATE: 2004-03-23
PRIOR FILING DATE: 1999-09-25
PRIOR FILING DATE: 1999-09-25
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARR: PATCHTIN VERSION 3.1
SEQ ID NO 5
LENGTH: 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKE
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Pred. No. 2.7e-23;
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APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2.609/6007-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23
PRIOR FILING DATE: 1998-09-24
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATCHIN VORBER: PCT/US99/22402
NUMBER: OF SEQ ID NOS: 7
SOFTWARE: PATCHIN VORBER: PCT/US99/22402
SEQ ID NO 4
SEQ ID NO 4
TURN OF SEQ ID NOS: 7
SOFTWARE: PATCHIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/10792311
Publication No. US20050038233A1
GENERAL INFORMATION:
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Best Local Similarity 89.5%;
Matches 77; Conservative
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ORGANISM: Artificial Sequence
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US-09-816-989A-4
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CURRENT FILING DATE: 2004-03-02

PRIOR PELLING DATE: 2001-03-23

PRIOR APPLICATION NUMBER: 06/101,693

PRIOR PELLING DATE: 1998-09-25

PRIOR APPLICATION NUMBER: PCT/US99/22402

PRIOR APPLICATION NUMBER: PCT/US99/22402
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GENERAL INCORANTION:
APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
TITLE Gad, NUCEULAR HEIGHTED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: COPOLYMER: 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REPERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT PILING DATE: 1998-09-25
PRIOR PILING DATE: 1998-09-25
PRIOR PELICATION NUMBER: PCT/US99/22402
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ilarity 89.5%; Pred. No. 2.7e-23;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 409; DB 17; Best Local Similarity 100.0%; Pred. No. 3.5e-28; Matches 86; Conservative 0; Mismatches 0;
61 YKAEAAKKAYKAEAAKAAAKEAAYEA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 YKAEAAKKAYKAEAAKAAAKEAAYEA 86
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                                                                                                                                                                      Sequence 6, Application US/10792311
Publication No. US20050038233A1
GENERAL INFORMATION:
APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 77; Conserv
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APPLICANT: Lis, DOTIS

TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKE
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/10/792,311
CURRENT APPLICATION NUMBER: US/09/816,989
PRIOR APPLICATION NUMBER: 00/101,693
PRIOR PILING DATE: 2001-03-25
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NOS: 7
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APPLICANT: Lis, Doris
IIILE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
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                                                                                                                                                                                ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
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Pred. No. 2.7e-13;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                 Score 233; DB 9;
Pred. No. 2.7e-13;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 YKAEAAKKAYKAEAAKAAAKEAAYEA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----YKAEAAKAAKEAYEA 56
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Publication No. US20050038233A1
GENERAL INFORMATION:
  PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.0%;
62.8%;
                                                                                                                               TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 62.8%;
Matches 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
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Matches 54; Conservative
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TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/10/792,311
CURRENT APPLICATION NUMBER: US/09/816,989
PRIOR APPLICATION NUMBER: US/09/816,989
PRIOR APPLICATION NUMBER: C0/101,693
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VERSION 3.1
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APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USB AS MOLECULAR WEIGHT MARK
FILLE OF INVENTION: COPOLYMER 1 RELATED FOR USB AS MOLECULAR WEIGHT MARK
FILLE OF INVENTION: AND FOR THERAPEUTIC USB
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILLING DATE: 2001-03-23
PRIOR PPLICATION NUMBER: 60/101,693
PRIOR FILLIG DATE: 1998-09-25
PRIOR PLICATION NUMBER: FCT/US99/22402
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                                                                                                                                                                                                                                      1 AKKYAKKEKAYAK-----AKKAEAK------AAKKAKAEAKKYAKAKAEKKEYAAAEAK 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-10-792-311-4
                        OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 20; Gaps
                                                                                                                                                          20;
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                                                                                                    65.5%; Score 268; DB 9; Length 66; 75.6%; Pred. No. 3.3e-16;
                                                                                                                                                       1; Indels
                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                  ------YKAEAAKAAAKEAYEA 66
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Patent No. US20020115103A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/10792311
Publication No. US20050038233A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT
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                                                                                                                                                    65; Conservative
                                                                                                                         Best Local Similarity
Matches 65; Conserv
                                              US-09-816-989A-4
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LENGTH: 66
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                                                                                                      Query Match
PEATURE:
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APPLICANT: Anderson, David
APPLICANT: Anderson, David
APPLICANT: Bogenberger, Jakob M.
APPLICANT: Beele, Bean R.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT SC
FILE REFERENCE: A-66900-4/RMS/AMS
CURRENT APPLICATION NUMBER: US 10/10/17,725
CURRENT FILING DATE: 1999-10-08
PRIOR PALICATION NUMBER: US 09/415,765
PRIOR PALICATION NUMBER: US 09/169,015
PRIOR PLILNG DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 173
SOFTWARES PATENTIAN OFFERENCE: ASSOCIATED ASSOCIATE
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APPLICANT: Anderson, David
APPLICANT: Bogenberger, Jakob M.
APPLICANT: Bogenberger, Jakob M.
APPLICANT: Bogenberger, Jakob M.
APPLICANT: Peele, Beau R.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT SC
CURRENT PAPLICATION NUMBER: US 10/10/393,449
CURRENT PAPLICATION NUMBER: US 10/177,725
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR PILING DATE: 1999-10-08
PRIOR PILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 173
SSG THARES PARENTED AND STRUCTURAL DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 173
SSC ID NO 20
LENGTH: 79
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Best Local Similarity 44.2%; Pred. No. 0.0047;
Matches 34; Conservative 16; Mismatches 1
                                            Sequence 20, Application US/10177725
Publication No. US20030143562A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20, Application US/10393449 Publication No. US20030224412A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 KEAEAKAKEAEAKAKEA 76
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ORGANISM: Artificial sequence
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ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: synthetic US-10-177-725-20
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; OTHER INFORMATION: synthetic
US-10-393-449-20
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US-10-393-449-20
              US-10-177-725-20
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TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REPERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/10/792,311
CURRENT FILING DATE: 2004-03-02
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR FILING DATE: 1998-09-25
PRIOR PILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATCHTIN VERSION 3.1
SEQ ID NO 3.7
LENGTH: 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
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45.3%; Pred. No. 0.0003;
tive 0; Mismatches 6;
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TITLE OF INVENTION: AND FOR THERAPEUTIC USE
CURRENT APPLICATION NUMBER: US(99/816,989A
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR PILING DATE: 1998-09-25
PRIOR PILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIAL OF THE SECOND NOW THE SECOND NOS: 7
SOFTWARE: PATENTIAL DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SEQ ID NO 2
LENGTH: 45
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Publication No. US20050038233A1
GENERAL INFORMATION:
APPLICANT: Gad, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
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Best Local Similarity 45.3%
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-816-989A-2
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US-10-1//-(2-15)
Sequence 15, Application US/1017725
Sequence 15, Publication No. US200301435621
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Anderson, David
APPLICANT: Beele, Beau R.
APPLICANT: Peele, Beau R.
TILE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT SC.
FILE REFERENCE: A-66900-4/RMS/AMS
CURRENT APPLICATION NUMBER: US/10/17,725
CURRENT APPLICATION NUMBER: US 09/415,765
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR FILING DATE: 1999-10-08
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 173
SOFTWARE: Patentin version 3.1
                                                    7
                                                                                                      7 KEKAYAKKAEKAAKKAEAKA----YKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAKYK 62
                                                                                                                                   ----AEAKKYAKAAKAEKKEYAAAEAKYKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15;
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28.2%; Score 115.5; DB 15; Length
39.8%; Pred. No. 0.0051;
tive 18; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: June 3, 2005, 11:47:09 Job time: 136 secs
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                                                                                                                                                                                                                                    64 EAAKKAYKAEAAKAAAKEAAYEA
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ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , OTHER INFORMATION: synthetic US-10-177-725-15
                                                    33; Conservative
  Query Match
Best Local Similarity
Matches 33; Conservat
                                                                                                                                                                                                                                                                                                                                RESULT 15
US-10-177-725-15
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| Sequence 19, Application US/2030224412A1
| Sequence 19, Application No. US20030224412A1
| GENERAL INFORMATION:
| APPLICANT: Andereon, David
| APPLICANT: Bogenberger, Jakob M.
| APPLICANT: Beale, Beau R.
| TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT FILE REFERENCE: RIGL-007CIP3
| CURRENT FILING DATE: 2003-03-18
| PRIOR PPLICATION NUMBER: US 10/177,725
| PRIOR APPLICATION NUMBER: US 09/415,765
| PRIOR APPLICATION NUMBER: US 09/415,765
| PRIOR APPLICATION NUMBER: US 09/169,015
| PRIOR PILING DATE: 1999-10-08
| NUMBER OF SEQ ID NOS: 173
| SEQ ID NO 19
| LENGTH: 86
                                                                                                                                                                                                                                                                 APPLICANT: Anderson, David
APPLICANT: Anderson, David
APPLICANT: Bogenberger, Jakob M.
APPLICANT: Beele, Beau R.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT (FILE REPERENCE: A-66900-4/RMS/AMS
CURRENT APPLICATION NUMBER: US/10/177,725
CURRENT APPLICATION NUMBER: US 09/415,765
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 173
SOFTWARE: Patentin version 3.1
SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 KEKAYAKKAEKAAKKAEAKA----YKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAKYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 28.2%; Score 115.5; DB 14; Length 86; Best Local Similarity 39.8%; Pred. No. 0.0051; Matches 33; Conservative 18; Mismatches 25; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 AEAAKKAYKAEA---AKAAAKEA 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 AKAAEAEAKAKAEAEAKAKAAEA 83
                                                                                                                                                                                                       Sequence 19, Application US/10177725 Publication No. US20030143562A1
                               70 YKAEA----AKAAKEA 82
                                                       :||| |:| ||||
60 KEAEAKAKEAEAKAKEA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial sequence
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COTHER INFORMATION: synthetic
US-10-177-725-19
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                                                                                                                                                                                                                                                         GENERAL INFORMATION
                                                                                                                                                   RESULT 13
US-10-177-725-19
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16642, A
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7, Appli
11, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/BCOMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-816-989A-6
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US-09-816-989A-4
US-09-816-989A-3
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US-09-816-989A-3
US-09-816-989A-3
US-09-816-989A-1
US-09-816-989A-1
US-09-816-989A-1
US-09-816-989A-1
US-09-816-989A-1
US-09-93-008A-6
US-08-93-008A-6
US-08-93-008A-6
US-08-93-108A-1
US-09-902-541-16
US-08-99-172-6
US-08-99-172-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
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                                                                                                                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
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No.
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Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 60, Appl Sequence 60, Appl Sequence 60, Appl Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl Sequence 14, Appl Sequence 16, Appl Sequence 17, Appl Sequence 12, Appl	SHT MARKERS	nce: SYNTHETIC Length 86; Indels 0; Gaps 0; KKYAKAAKAEKKEYAAAEAK 60                     KKYAKAAKAEKKEYAAAEAK 60
US-08-898-300-17 US-08-808-300-17 US-08-460-890A-60 US-08-460-91A-60 US-08-460-91A-60 US-08-460-91A-60 US-08-902-540-14758 US-08-902-540-14758 US-08-902-540-14758 US-08-303-025-15 US-08-677-304-13 US-08-677-304-13 US-08-677-304-13 US-08-677-304-13 US-08-83-703B-2 US-08-93-703B-4	ALIGNMENTS  ULT 1  09-405-743A-6  109-405-743A-6  109-405-743A-6  ENERAL INFORMATION:  ENERAL INFORMATION:  ENERAL INFORMATION:  ENERAL INFORMATION:  GLATIRAMER ACETATE MOLECULAR WEIGHT  FILE REFERENCE: 60807-A  FILE REFERENCE: 60807-A  FULE REPERENCE: 1999-09-24  NUMBER OF INFORMATION NUMBER: US/09/405,743A  GURRENT FILING DATE: 1999-09-24  NUMBER: PATHOLICATION NOS: 7  OSPTWARE: PATHOLICATION OF: 2.1  EQ ID NO 6  LENGTH: 86  TYPE: PRT  ORGANISM: Artificial Sequence  FEATURE:	of Artificial Seque Score 409; DB 4; Pred. No. 3.2e-31; Mismatches 0; ARAKAYKAAEAKKKAKAEA                     GABAKAYKAAEAKKKAKAEA GABAKAYKAAEAKKKAKAEA
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	ALL 6 6 6 6 6	Description PEPTIDE 100.0%; 100.0%; vative 0; vative             AYAKKAEKAAKI AYAKKAEKAAKI AYAKKAEKAAKI AYAKKAEKAAKI AYAKKAEKAAKI AYKAEAAKAAAKI XKAEAAKAAAKI
20000000000000000000000000000000000000	i. 743A-6 i.e. 6, Application US/ i.e. 6, Application US/ i.e. 1.e. 1.e. 1.e. 1.e. 1.e. 1.e. 1.e.	INFORMATION: DESCRI- INFORMATION: PEPTID 743A-6 LCh al Similarity 100 al Similarity 100 al AKKYAKKEKAYAKKA 1 AKKYAKKEKAYAKKA 1 AKKYAKKEKAYAKKA 61 YKAEAAKKAYKAEAA 61 YKAEAAKKAYKAEAA 61 YKAEAAKKAYKAEAA
0 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	RESULT 1  US-09-405-743A-6  Sequence 6, Applicat Patent No. 614938  GENERAL INFORMATION: PAPLICANT: Yeda Re TITLE OF INVENTION: PILE REFERENCE: 60 CURRENT APPLICATION CURRENT FILING DATE NUMBER OF SEQ ID NO SOFTWARE: PATENTING SOFTWARE: PATENTING LENGTH: 86 LENGTH: 86 TYPE: PRT TYPE: PRT PRATURE: PREMURES: ARLIFICI	INFO INFO -743A atch cal S 61 1
2 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 US-09-405-74; Sequence 6 Sequence 6 GENERAL INE TITLE OF 1 FILE REFER CURRENT AF CORGANISM CORGANISM	CTHER COTHER COTHER COLORY M BEST LO BATCHES COY COY

Sequence 6, Application US/09816989A

Patent No. 6800287

GRNERAL INFORMATION:
APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKE
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 1998-09-25
FRIOR PILING DATE: 1998-09-25
FRIOR PILING DATE: 1999-09-24
PRIOR FILING DATE: 1999-09-24

US-09-816-989A-6

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Sequence 4, Application US/09816989A

Patent No. 6800287

CREERAL INFORMATION:
APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKI
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
TITLE REFERENCE: 2609/60807-A-PCT-US
CURRENT PAPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR APPLICATION NUMBER: POT/US99/22402
PRIOR PILING DATE: 1999-09-24
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                                                                                                                                                         ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-5
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Patent No. 5514938
GENERAL INFORMATION:
APPLICANT: YeaR Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
                                                                                                                                                                                                                                                         77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 66;
                                                                                                                                                                                                                                                       Score 351.5; DB 4; Length
Pred. No. 5.8e-26;
0; Mismatches 0; Indels
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; OTHER INFORMATION: Description of Artificial Sequence:

; OTHER INFORMATION: PEPTIDE

US-09-405-743A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 60807-A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SEQ ID NO 4
LENGTH: 66
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                            SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 77
                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 89.5%;
Matches 77; Conservative
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       NUMBER OF SEQ ID NOS: 7
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Best Local Similarity
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US-09-405-743A-4
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Matches
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                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
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TITLE OF INVEXTYON: GLATTRAMER ACETATE MOLECULAR WEIGHT MARKERS
ELLE REFERENCE: 608074
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 2.1
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                                                                                                                                                                                                                                                         Score 409; DB 4; Length 86;
Pred. No. 3.2e-31;
                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                           0; Mismatches
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                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%;
Matches 86; Conservative 0;
NUMBER OF SEQ ID NOS: 7
SOFWARE: Patentin version 3.1
SEQ ID NO 6
LENOTH: 86
                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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LENGTH: 77
                                                                                                                                                      FEATURE:
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GENERAL INFORMATION:

APPLICANT: Gad, Alexander

APPLICANT: Gad, Alexander

APPLICANT: Gad, Alexander

APPLICANT: Gad, Alexander

APPLICANT: Lis, Doria

TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKE

TITLE OF INVENTION: AND FOR THERAPEUTIC USE

TITLE OF INVENTION: AND FOR THERAPEUTIC USE

CURRENT APPLICATION NUMBER: US/09/816,989A

CURRENT APPLICATION NUMBER: 60/101,693

PRIOR APPLICATION NUMBER: 60/101,693

PRIOR APPLICATION NUMBER: PET/US99/22402

PRIOR PILING DATE: 1999-09-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAABAKKKKAEAK ------39
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                                                                                                                                                                          ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-3
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Sequence 2, Application US/09405743A

Patent No. 6514938

GENERAL INFORMATION:
APPLICAMT: Yead Research and Development Co., Ltd.

APPLICAMT: Yead Research and Development Co., Ltd.

TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS

FILE REFERENCE: 60807-A

CURRENT APPLICATION NUMBER: US/09/405,743A

CURRENT PILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 2.
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30.9%; Score 126.5; DB 4; Length 45;
Best Local Similarity 45.3%; Pred. No. 1.9e-05;
Matches 39; Conservative 0; Mismatches 6; Indels 4.
                                                                                                                                                                                                                                                                               Query Match 57.0%; Score 233; DB 4; Length 56; Best Local Similarity 62.8%; Pred. No. 3.6e-15; Matches 54; Conservative 2; Mismatches 0; Indels
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NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 56
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ORGANISM: Artificial Sequence
                                                                                                                   TYPE: PRT ORGANISM: Artificial Sequence
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APPLICANT: Gad, Alexander

APPLICANT: List, Doris

TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK

TITLE OF INVENTION: AND FOR THERAPEUTIC USE

FILE REFERENCE: 2609/60807-A-PCTT-US

CURRENT APPLICATION NUMBER: 60/101,693

PRIOR APPLICATION NUMBER: 60/101,693

PRIOR APPLICATION NUMBER: PCT/US99/22402

PRIOR APPLICATION NUMBER: PCT/US99/22402
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Patent No. 6514938
GENERAL INFORMATION:
APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS FILE REFERENCE: 60807-A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEG ID NO 3
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  NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 66
                                                                                                                      TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity 62.8'
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Best Local Similarity 57.9%; Pred. No. 0.00011;
Matches 33; Conservative 6; Mismatches 17; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-816-989A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                            1 AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAK 60
                                                                                                                                      ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-2
                                                                                                                                                                                                                                         41; Gaps
                                                                                                                                                                                               Length 45;
                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,008A
FILING DATE: 18-DEC-1997
CLASSIFICATION: 514
                                                                                                                                                                                             Score 126.5; DB 4;
Pred. No. 1.9e-05;
0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                     1 AKKYAKK-----AKAEKA-----KKAYKAAEAKKAAKYE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 5370 Manhattan Circle, Suite 201
STREET: Creenlee, Winner and Sullivan
CITY: Boulder
STATE: CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polycationic Oligomers
                                                                                                                                                                                                                                                                                                                                                          61 YKAEAAKKAYKAEAAKAAAKEAAYEA 86
                                                                                                                                                                                                                                                                                                                                                                                               ------KAAAEKAAKEAAYEA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032,436
FILING DATE: 18-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 32,064
REFERENCE/DOCKET NUMBER: 33-95
TELECOMUNICATION:
TELEPHONE: 303-499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/08993008A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SS: not relevant not relevant
                  SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 45
                                                                                                                                                                                               30.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liotta, Dennis C.
                                                                                      ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Petros, John A. APPLICANT: Wey, Shiow-Jyi APPLICANT: Karr, Joan F. TITLE OF INVENTION: Polycat NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Sullivan, Sally A. REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 56 amino acids
                                                                                                                                                                                               Query Match
Best Local Similarity 45.33
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   303-499-8089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 6153596
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80303
                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
US-08-993-008A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                          ò
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Length 56;

29.2%; Score 119.5; DB 3;

Query Match

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Sequence 1, Application US/09816989A

Sequence 1, Application US/09816989A

Patent No. 6800287

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Lis, Doris

TITLE OF INVENTION:

TITLE OF INVENTION: AND FOR THERAPEUTIC USE

FILE REFERENCE: 2609/60807-A-PCT-US

CURRENT APPLICATION NUMBER: US/09/816,989A

CURRENT APPLICATION NUMBER: 60/101,693

PRIOR PILING DATE: 1998-09-25

PRIOR PILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
1; Gaps
                                                  9 KAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYNTHETIC
                                                                                                                                                                                                                                                                                                                  APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AKKYAKKEKAAKKAY-----KKEAKAKAAEAAKEAAYEA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AKKYAKKEKAAKKAY-------KKEAKAKAABAAKEAAYEA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26.4%; Score 108; DB 4; Length 35; 57.4%; Pred. No. 0.00074; ive 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26.4%; Score 108; DB 4; Length 35; 57.4%; Pred. No. 0.00074; Live 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40 AKKYAKAKAEKKEYAAAEAKYKAEAAKKAYKAEAAKAAKEAAYEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 35
                                                                                                                                                                                                                                      Sequence 1, Application US/09405743A Patent No. 6514938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 57.4
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 57.4
Matches 27; Conservative
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Patent No. 5670483
GENERAL INFORMATION:
CALLS
APPLICANT: Zhang, Shuguang
APPLICANT: Lockshin, Curtis
APPLICANT: Rich, Alexander
APPLICANT: Holmes, Todd
TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
TITLE OF INVENTION: THEREFOR
TITLE OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROCK, SMITH & REYNOLDS, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 KAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAKYKAEA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
26.0%; Score 106.5; DB 3; Length 48;
Best Local Similarity 59.2%; Pred. No. 0.0014;
Matches 29; Conservative 6; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,008A FILING DATE: 18-DEC-1997
CLASSIFICATION DATA: 06/032,436 PRIOR APPLICATION DATE: 06/032,436 PRIOR APPLICATION DATE: 18-DEC-1996 ATTORNEY/AGENT INFORMATION: NAME: 30.114van, Sally A. REGISTRATION NUMBER: 32,064 REPRENCE/POCKET UNBER: 33.95
TELECOMMUNICATION INFORMATION: TELECOMMUNICATION: TELECOMMUNICATI
                                                                                                                                                                                                                                                                     APPLICANT: Petros, John A.
APPLICANT: Wey, Shiow-Jyi
APPLICANT: Wey, Shiow-Jyi
APPLICANT: Wey, Shiow-Jyi
APPLICANT: Wey, Shiow-Jyi
APPLICANT: Fohl, Jan
TITLE OF INVENTION: Polycationic Oligomers
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                       Sequence 5, Application US/08993008A
Patent No. 6153596
GENERAL INFORMATION:
APPLICANT: Liotta, Dennis C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
OLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 303.499-8089
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
LENGTH: 48 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ANTI-SENSE: NO
US-08-993-008A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 80303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-346-849-16
RESULT 14
US-08-993-008A-5
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STREET: Two Militia Drive

CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.A.
2179: 02173-4799
COUNTRY: U.S.A.
2179: 02173-4799
COUNTRY: U.S.A.
2179: 02173-4799
COUNTRY: U.S.A.
2179: 02173-4799
COMPUTER: READABLE FORM:
COMPUTER: THE PORT COMPANIENT PRE-BASE #1.0, Version #1.25
COMPUTER: THE POSS #1.0, Version #1.0, Vers
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

3, 2005, 11:43:56 ; Search time 39 Seconds (without alignments)
268.914 Million cell updates/sec Run on:

US-10-792-311-7 519 Title: Perfect score:

1 AKKYAKKAEKAYAKKAKAKAK.......AKAYKAEAAKAAAKEAAYEA 109 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 109

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STRMMARTES

SUMMARIES	Description	.0	histone H1-			-	7 hypothetical prote			sperm-specific			hypothetical		micro glutam											4 protamine phi-3.2			S another months EME	
S	£	G60110	819915	H64327	H81072	NSCHH4	T30977	802720	S04157	865494	B75029	806918	T26945	G81080	QFBO	T38936	S44095	A33310	FDFL4W	S04941	834115	802376	S10545			S10544	NSTR6		821225	
	08	2	7	Н	~		~	~	0	7	7	~	7	~	_	~	~	7	7	~	7	7	~					7		
	Length	97	103	104	86	105	62	88	93	101	108	78	81	107	82	108	98	100	82	45	92	97	45		100			87	101	
d	Query Match	21.9	19.6	18.2	18.1	17.8	17.7	17.6	17.5	17.1	17.1	16.5	16.5	16.5	16.1	16.0	15.7	15.6	15.1	15.0	15.0	14.5	14.5	14.5	14.4	14.3	14.3	14.1	14.1	
	Score	113.5	101.5	94.5	94	92.5	92	91.5	91	89	89	85.5	85.5	'n	83.5	83	81.5	81	78.5	78	78	75.5	75	75	74.5	74	74	73	73	
	Result No.	-	7	М	4	2	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	

nonhistone chromos antifreeze protein	nonhistone chromos	embryonic abundant	nonhistone chromos	nonhistone chromos	nonhistone chromos	nonhistone chromos	hypothetical prote	hypothetical prote	protein F1504.29 [	nonhistone chromos	H+-transporting tw	ribosomal protein	probable secreted	histone H1.1 - bov
A26989 A22592	S11349	523528	833866	803700.	S11219	JU0038	H95245	E98110	C86477	NSBOH7	T45101	A75410	AD0682	HSB011
0 0	~	N	N	N	~	N	~	N	N	-	N	N	N	-1
100	88	104	89	90	96	66	103	103	107	83	109	92	93	105
13.8	13.4	13.4	13.3	13.3	13.2	13.2	13.2	13.2	13.2	13.1	13.0	12.9	12.9	12.9
71.5	69.5	69.5	69	69	68.5	68.5	68.5	68.5	68.5	68	67.5	67	29	67
30	32	33	34	35	36	37	38	39	40	41	42	43	44	45

repetitiv	repetitive protein antigen 69/70 - Trypanosoma cruzi (fragment)
C;Specier C;Date: ]	C;Species: Trypanosoma cruzi C;Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 09-Jul-2004
C; Access: R; Hoft, I	C;Accession: G60110 R;Hoft, D.F.; Kim, K.S.; Otsu, K.; Moser, D.R.; Yost, W.J.; Blumin, J.H.; Donelson, J.E.;
Infect.	manners 57, 1959-1967, 1989
A; Referer	Ajittie: irypanosoma cruzi expresses diverse repetitive procein dicigens. XX Reference number: A60110; MUID:89277508; PMID:2659529 XX XX COCCION: CE0110
A; Status	A;Status: not compared with conceptual translation
A; Molecu.	A;Molecule type: mRNA A;Residues: 1-97 <hof></hof>
A; Cross-1	A, Cross-references: UNIPROT: Q7M3W1
C; Superior C; Keyword	C;Supertamily: Vailcella-zoster Virus gene ZZ protein C;Keywords: tandem repeat
F;1-85/Re	F;1-85/Region: 7-residue repeats
Query 1	Match 21.9%; Score 113.5; DB 2; Length 97;
Matche	best notar similarity 17.3%; Fred: NO. 0.33% Matches 43; Conservative 1; Mismatches 42; Indels 5; Gaps 2;
ò	16 AKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEAYKAEAKKYAKAAKAE 75
qq	1 AAPAKAAAAPAKAAAAPAKAAAAPAKAAAAPAKAAAAPAKAAAAPAKAAAAPA 59
ò	76 KKEYAAAEAKKAEAAKAYKAEAAKAAAKEAA 106
a a	

Distone H1-like protein - tomato (fragment)
C;Species: Lycopersicon esculentum (tomato)
C;Species: Lycopersicon esculentum (tomato)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: S19915
R;Bray, E.A.; Moses, M.S.; Cohen, A.; Imai, R.; Plant, A.L.
submitted to the EMBL Data Library, March 1992
A;Description: Regulation during environmental stress of an H1 histone-like gene by endog A;Reference number: S19915
A;Reference number: S19915
A;Rocession: S19915
A;Roslecule type: mRNA
A;Residues: 1-103 - KBA>
A;Residues: 1-103 - KBA>
C;Superfamily: histone H1

5 Gaps Query Match 19.6%; Score 101.5; DB 2; Length 103; Best Local Similarity 35.0%; Pred. No. 2.1; Matches 35; Conservative 8; Mismatches 50; Indels 7

```
hypothetical protein C01B10.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 AEGEAKEEPKRRSARLSA---KPAPPKPEPKPKKAAPKKEKAANDKKEDKKAATKGKKGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 YKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 KGKDETKQEDAKEENHSENGDTKTNEAPAAEASDDKEAKS 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession: T30977

R; Blanchard, M.; Bradshaw, H.

Submitted to the EMBL Data Library, August 1999

A; Description: The sequence of C. elegans cosmid C01B10..

A; Reference number: Z20949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Accession: T30977
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-62 <BLA>
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                                   94 KAEAAKAAAKEA-AYEA 109
                                                                                         75 EAPAAEAATEAPAAEA 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 2-5;16-42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dypothetical protein NMB1523 [imported] - Neisseria meningitidis (strain MC58 serogroup C; Species: Neisseria meningitidis
R; Tettelin, H: Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H:; Qin, H:; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A; Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A; Reference number: A81000; MUID:20178755; PMID:10710307
A; Accession: H81072
A; Molecule type: DNA
A; Residues: 1-98 < TET.
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A,Experimental source: serogroup B, strain MC58
                                                                                                                                                                                                                                                                                                                             Conserved hypothetical protein MJ0223 - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: H64227
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R; Reich, C.J.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Reich, C.J.; Joverbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.A.; Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii A;Reference number: A64300; MUID:96337999; PMID:8688087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cross-references: UNIPROT: Q57676; GB: U67478; GB: L77117; NID: 91590958; PIDN: AAB98215.1
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   69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: REV214474-214160
C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 KAAEAKKKAKAEAKKYAKEAAKAKKEAYKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAY 93
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                                                         3 AAKGKLIKIKASYKLSEAGKKETTTKTSTKKLPKADSKKKPRSTRATSTAAKKTEVPKKA
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                                                                                                                                                                KAAKAEKKEYAAAEAK----KAEAAKAYKAEAAKAAKEA 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18.2%; Score 94.5; DE 37.0%; Pred. No. 5.8; tive 11; Mismatches
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Pred. No. 6;
4; Mismatches
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64 EEEAKKEAEKILEETEKEIKE
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Best Local Similarity 50.6%;
Matches 39; Conservative 4
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Matches 30; Conservative
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A;Molecule type: DNA
A;Residues: 1-105 <BRO>
A;Cross-references: UNIPROT: P12902; EMBL:X63086
R;Cross-references: UNIPROT: P12902; EMBL:X63086
Gane 63, 287-295, 1988
A;Title: Chicken chromosomal protein HMG-14 and HMG-17 cDNA clones: isolation, character;
A;Reference number: JT0283; MUID:8825874; PMID:3384337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ribrowne, D.L.; Dodgson, J.B.
Gene 124, 199-206, 1993
A;Title: The gene encoding chicken chromosomal protein HMG-14a is transcribed into multig
A;Reference number: JU0140; MUID:93185924; PMID:8444343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Cross-references: EMBL:X63083
C;Comment: The HMG proteins are small nonhistone chromosomal proteins, rich in both basic
C;Comment: This protein is apparently one of the necessary components of actively transco
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nonhistone chromosomal protein HWG-14a - chicken N'Alternate names: high mobility group protein-14a . C'Species: Gallus gallus (chicken) C'Species: Gallus gallus (chicken) C'Species: Gallus 130-14n-1999 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004 C'Accession: S22122; JT0282; JT0140 R'Browne, D.L.; Dodgson, J.B. Gubmitted to the EMBL Data Library, November 1991 A;Description: The chicken HMG-14a gene is transcribed into multiple mRNAs. A;Reference number: S22122
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A,Molecule type: mRNA
A,Residues: 2-105 -000>
A,Cross-references: GB:M26675; NID:g211920; PIDN:AAA48815.1; PID:g211921
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C;Keywords: chromosomal protein; DNA binding; nucleus
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C;Accession: B75029
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struct, A;Reference number: A75001
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A;Rosidues: 1-108 «KAM»
A;Cross-references: UNIPROT:Q9UXU1; GB:AJ248288; GB:AL096836; NID:g5458960; PIDN:CAB5067;
A;Experimental source: strain Orsay
                                                                                                                                                                                                                                                                                                                                                                      A,Title: Complete sequence and characterization of the major sperm nuclear basic protein A,Reference number: S65494; MUID:95246879; PMID:7729549
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C;Species: Holothuria tubulosa
C;Species: Peb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C;Accession: S06918
R;Prats, E.; Cornudella, L.; Ruiz-Carrillo, A.
                                                                                                                                                                                    sperm-specific protein PL-III - North Pacific mussel
C;Species: Mytllus trossulus (North Pacific mussel)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S6549, P.; Ausio, J.
FEBS Lett. 363, 37-40, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Residues: 1-101 <ROC>
A;Cross-references: UNIPROT:Q9TXE3; PIDN:AAB34147.1; PID:g998687
C;Keywords: chromosomal protein; DNA binding; nucleosome; sperm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 17.1%; Score 89; DB 2; Length 101; Local Similarity 25.0%; Pred. No. 13; length 101; les 26; Conservative 27; Mismatches 43; Indels
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-----YAKAAKAEKKEYAABAKK
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A, Status: preliminary
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A,Gene: PAB1179
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Matches
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R;Woods, J.P.; Spinola, S.M.; Strobel, S.M.; Cannon, J.G.
Mol. Microbiol. 3, 43-48, 1989
A;Title: Conserved lipoprotein H.8 of pathogenic Neisseria consists entirely of pentaper
A;Reference number: S02720; MUID:89237899; PMID:2497298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Molecule type: DNA
A,Residues: 1-88 <WOO>
A,Residues: 1-88 <WOO>
A,Cross-references: UNIPROT:P11910; EMBL:X12627; NID:g44863; PIDN:CAA31145.1; PID:g44864
C,Keywords: membrane protein
F,1-17/Domain: signal sequence #status predicted <SIG>
P,18-88/Product: outer membrane protein H.8 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encodes 14 tandemly repeated penta
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                                                                                                                                                                                                                                                                                    7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 KKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEAYKAEAKKYAKAK 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 KKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEAYKAEAKKYAKAAK 73
                                                                                                                                                                                                                                                                                                                                                11 AYAKKAKAAKEKKAYAKKEAKAYKAAEA--KKKAKAEAKKYAKEAAKAKKEAYKAEAKK 67
                                                                                                                                                                                                                                                                                                                                                                                3 AVQKAKKVAKTKKVAAKPKAPKVKKIQASPKKAAAPKAKKPVKKAAAKKSPAKKAPPKK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              outer membrane protein H.8 precursor - Neisseria gonorrhoeae
C;Species: Neisseria gonorrhoeae
C;Date: 18-Oct_1989 #sequence_revision 18-Oct-1989 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-Dec-1992 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                       5
         A;Cross-references: UNIPROT:Q17536; EMBL:U58757; PIDN:AAC47916.1
A;Experimental source: strain Bristol N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
17.6%; Score 91.5; DB 2; Length 88;
Best Local Similarity 43.0%; Pred. No. 7.9;
Matches 40; Conservative 9; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 17.5%; Score 91; DB 2; Length 93; Best Local Similarity 38.7%; Pred. No. 8.9; Matches 36; Conservative 10; Mismatches 45; Indels
                                                                                                                                                                                                                    Score 92; DB 2; Length 62;
Pred. No. 5.7;
4; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          outer membrane protein H.8 precursor - Neisseria gonorrhoeae
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R; Baehr, W.; Gotschlich, E.C.; Hitchcock, P.J.
Mol. Microbiol. 3, 49-55, 1989
A; Title: The virulence-associated gonococcal H.8 gene en A; Reference number: S04157; MUID:89237900; PMID:2497299
A; Accession: S04157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74 AEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAA 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C,Species: Neisseria gonorrhoeae
C,Date: 04-Dec-1992 #sequence_revision
                                                                                                                                                                                                                    Query Match 17.7%;
Best Local Similarity 45.8%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Keywords: membrane protein
                                                                                            A; Map position: IV
A; Introns: 27/3; 61/3
A; Note: C01810.5
                                                                         C;Genetics:
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us-10-792-311-7.rpr

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FEBS Lett. 182, 389-392, 1985
A,Title: Brain micro glutamic acid-rich protein is the C-terminal endpiece of the neurofi
A,Reference number: A02964, MUID:85154567, PMID:3884373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                f the L protein.

C;Comment: Although there are, as yet, no known biological functions ascribed to this protein cytoplasmic neuronal transport occurring in the presence of calcium ion and possibly t; Superfamily: cytoskeletal keratin
C;Keywords: brain; coiled coil; cytosol; intermediate filament
F;1-82/Domain: neurofilament triplet L protein tail subdomain b (fragment) <SIG>
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A;Cross-references: UNIPROT:P87057; EMBL:Z94864; PIDN:CAB08172.1; GSPDB:GN00066; SPDB:SP?
A;Experimental source: strain 972h-; cosmid c57A10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: protein A;Molecule type: protein A;Mosidues: 1-82 -150>. C;Comment: This acidic protein, isolated from the cytosolic fraction of brain tissue, cor C;Comment: The similarity of this sequence to part of the neurofilament triplet L proteir C;Comment: The similarity of this sequence to part of the neurofilament triplet L proteir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               non-listone chromosomal protein high mobility group - fission yeast (Schizosaccharomyces C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 16-Aug-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       micro glutamic acid-rich protein - bovine
N'Alternate names: neurofilament triphet L protein (fragment)
C.Species: Bos primigenius taurus (cattle)
C.Pate: 28-May-1986 #sequence_revision 28-May-1986 #text_change 22-Nov-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 AKKAKAAKEKKAYAKKEAKAYK------AAEAKKKAKAEAKKYAKEAAKAKEAYKA
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**Radcock, K.; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, April 1997
A; Reference number: Z21818
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                                                                                                                                   Length 107;
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                                                                                                                                                                                                                                                                                                                                                                                               64 EAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAA---KEAA 106
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16.1%; Score 83.5; DB 1; Length 82
Best Local Similarity 32.4%; Pred. No. 24;
Matches 24; Conservative 19; Mismatches 30; Indels
                                                                                                                                                                                                   34; Indels
                                                                                                                                   DB 2;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                   Query Match
16.5%; Score 85.5; Di
Best Local Similarity 34.9%; Pred. No. 22;
Matches 37; Conservative 12; Mismatches
   A, Experimental source: serogroup B, strain MC58 C, Genetics:
A, Gene: NMB1468
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A;Introns: 44/1; 63/3
C;Superfamily: HMG box homology
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R; Isobe, T.; Okuyama,
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C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: G81080
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.B.; Eisen, J.A.Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Pleischmann, R.D.; Dougherty, B.A.; it, H.; Oin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Authors: Grandl, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A;Tille: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
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A,Residues: 1-107 <TET>
A,Cross-references: UNIPROT:Q9JYR2; GB:AE002496; GB:AE002098; NID:g7226701; PIDN:AAF4182
                              A;Title: Nucleotide sequence of a cDNA for phi(0), a histone to protamine transition pro
A;Reference number: S06918; MUID:90098774; PMID:2602115
A;Accession: S06918
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A;Experimental source: clone Y45F3A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein Y45F3A.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T26945
R;Steward, C.
submitted to the EMBL Data Library, October 1998
A;Reference number: Z20289
A;Accession: T26945
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                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-78 ePRA>
A;Cross-references: UNIPROT:P14309; EMBL:X16364; NID:g9461; PID:g9462
C;Keywords: DNA binding
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A;Molecule type: DNA
A;Residues: 1-81 <WIL>
A;Cross-references: UNIPROT:Q9XWY9; EMBL:AL032621;
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Nucleic Acids Res. 17, 10097, 1989
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Les 33; Conservative
                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 24; Conserv
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A;Status: preliminary
A;Molecule type: DNA
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Query Match
Best Local Similarity 27.1%; Pred. No. 32;
Matches 29; Conservative 22; Mismatches 38; Indels 18; Gaps 4;
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Copyright (c) 1993 - 2005 Compug
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SEQUENCE FROM N.A.

STRAIN=CRA009 / ATCC BAA-98;

STRAIN=CRA009 / ATCC BAA-98;

Pubmed=14704707; DOI=10.1038/nbc923;

Pubmed=14704707; DOI=10.1038/nbc923;

A Laximer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L.,

Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,

Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Peres C.,

Harrison F.H., Gibson J., Harwood C.S.;

"Complete genome sequence of the metabolically versatile

photosynthetic bacterium Rhodopseudomonas palustris.";

Nat. Biotechnol. 22:55-61(2004).

R. BEMBL; BX572603; CAE28621.1;

GO; GO:0003634; Cinucleosome; IEA.

GO; GO:0003677; F:DNA binding; IEA.

GO; GO:0003677; F:DNA binding; IEA.

R. InterPro; IPR005819; Histone—H5.
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Q95un5 t
P40268 t
Q93mu2 p
P40270 t
Q93mu4 e
Q93mu4 e
Q93mu4 e
Q95q20 c
Q95q20 c
                                    093mu8
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Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Bradyrhizobiaceae, Rhodopseudomonas.
NCBI_TaxID=1076;
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Pred. No. 0.0054;
7; Mismatches 28; Indels
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Complete protecme; Hypothetical protein.
SEQUENCE 105 AA; 11042 MW; CEDB59B3D937E980 CRC64;
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                                                H161 TRYCR
Q95UN5
H1C2 TRYCR
Q93MU2
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093MU4
093MU5
090N6K5
090NFK0
095QZ0
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Best Local Similarity 52.7%;
Matches 48; Conservative
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nuclear protein

Name=lnp18;

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Aglagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D., Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B., Biking T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M., Dui D., Ianakiev P., Pedersen D., Nelson M., Washburne M., Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U., Rothe G.O., Jedd G., Newses W., Staben C., Marcotte E., Greenberg D., Roy A., Foley K., Naylor J., Manceli E., Bielke C., Rudd S., Frishman D., Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S., Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A., DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R., Yarden O., Plamann M., Seiler S., Dunlap J., Rafford A., Aramayo R., Natvig D.O., Alex L.A., Namnhaupt G., Ebbone D.J., Freitag M., Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B., The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 KKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEAY 61
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NCBI_TaxID=5659;
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-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                  Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                      94 AA.
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GO; GO:0000786; C:nucleosome; IEA.
GO; GO:0005634; C:nucleos; IEA.
GO; GO:0003674; F:DNA binding; IEA.
GO; GO:0003674; F:DNA binding; IEA.
                                                                                                                                                                                                            Created)
                                                                                                                              PRT;
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Matches 31; Conservative
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                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                         Q7SD04;
01-MAR-2004
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Q9BMY8;
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MEDLINE=2226343; PubMed=12438377;

DOI=10.1128/IAI.70.12.6976-6986.2002;

Papageorgiou F.T., Socraiadou K.P.;

Expression of a novel Leishmania gene encoding a histone H1-like, protein in Leishmania major modulates parasite infectivity in vitro.";

Infect. Immun. 70:6976-6986(2002).

EMBL; AJ237814; CAD21431.1;

GO; GO:0000786; C:nucleosome; IEA.

GO; GO:0005634; C:nucleosome; IEA.

GO; GO:000384; P:nucleosome assembly; IEA.

PRINTS; PRO0624; HISTONEHS.
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MEDLINE=22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.;
Leishmania major.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
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.., iriguchi M., Wada T., Yamada
.., iriguchi M., Wada T., Yamada
.., iriguchi M., Wada T., Yamada
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
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Last annotation update)
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Pred. No. 0.037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 KEAYKAEAKKYAK--AAKAEKKEYAAAEAKK 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 KPAKKA-AKKPAKKPAKKAAKKAAKK 98
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Matches 51; Conserv
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[2]
SEQUENCE FROM N.A.
STRAIN=Friedlin;
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NCBI_TaxID=5664;
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STRAIN=Friedlin;
MEDLINE=94187808; PubMed=8139626; DOI=10.1016/0166-6851(93)90123-F;
Fasel N.J., Robyr D., Mauel J., Glaser T.A.;
"Identification of a histone H1-like gene expressed in Leishmania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=LV39;
MEDLINE=94187808; PubMed=8139626; DOI=10.1016/0166-6851(93)90123-F;
Pagel N.J. Robyr D.C., Mauel J., Glaser T.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fasel N.J., Robyr D.C., Mauel J., Glaser T.A.,
"Identification of a histone H1-like gene expressed in Leishmania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22.9%; Score 119; DB 2; Length 105; 43.0%; Pred. No. 0.7;
                                                                                                                                                                     Match 23.1%; Score 120; DB 2; Length 96; Local Similarity 41.0%; Pred. No. 0.56; es 34; Conservative 9; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29; Indels
Melo G.S., Fragoso S.P., Fasel N.S., Mendonca S.C.F.; Submitred (DEC-202) to the EMBL/GenBank/DDBJ databases. EMBL; AF207632, 2AAG6608.2; SEQUENCE 96 AA; 9893 MM; AAE604694F9F6205 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mol. Biochem. Parasitol. 62:321-323(1993).
EMBL; U01031; AAA18635.1; -.
SEQUENCE 105 AA; 10909 MW; D8C32835131ACF38 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Histone H-1 like protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       105 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 EAKKYAKAAKAEKKEYAAAEAKK 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 -VKKVVKAVKTAKKSSKKSSAKK 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=SW3.1; Synonyms=sw3.0;
Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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Eukaryota, Euglen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=5664;
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                                                                                                                                                                     Query Match
Best Local S
Matches 34
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Matches
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3 KYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKAYK 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Trypanosoma cruzi.
Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
MEDLINE=97237563; PubMed=9084041; DOI=10.1016/S0166-6851(96)02801-0; Noll T., Desponds C., Jacquet R., Belli S., Fasel N.J.; T. Desponds R. Jacquet, S. Belli and N. J. Fasel. Histone N. Moll, C. Desponds, R. Jacquet, S. Belli and N. J. Fasel. Histone Hil expression varies disting Leishmania majordevelopment."; Moll. Biochem. Parasitol. 84:215-227(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hoft D.F., Kim K.S., Otsu K., Moser D.R., Yost W.J., Blumin J.H., Donelson J.E., Kirchhoff L.V.; "Trypanosoma cruzi expresses diverse repetitive protein antigens."; Infect. Immun. 57:1959-1967(1989).
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Pred. No. 1.5;
1; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                           Score 118; DB 2; Length 105;
Pred. No. 0.81;
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                                                                                                                                                                                                                             Fasel N.J.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                  DUBLI, AJ223861; CAA11592.1; -.
EMBL, AJ223860; CAA11591.1; -.
EMBL, AJ233860; CAA11591.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97 AA; 8210 MW; 477B46BEE0DFE3E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Repetitive protein antigen 69/70 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 KKEYAAAEAKKAEAAKAYKAEAAKAAAKEAA 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 -- VKKVVKAVKTAKKSSKKSSAKK 105
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MEDLINE=89277508; PubMed=2659529;
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                                                                                                                                                                                                                                                                                                                                                                                        ch 22.7%;
1 Similarity 41.7%;
35; Conservative
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SEQUENCE FROM N.A. STRAIN=Tulahuen 2;
                                                                                                                                                    Irypanosoma cruzi
                                                                                                                                       Histone H1.M6.2
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                                                                               TRYCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62
                                                                               H162 TRY
P40274;
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                                                                   H162_TRYCR
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                                                                                                     Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=31285;
                                                                                                                                                                                                                                                                                                              12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermus thermophilus (strain HB27 / ATCC BAA-163 / DSM 7039).
Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Henne A., Brueggemann H., Raasch C., Wiezer A., Hartsch T., Liesegang H., Johann A., Lienard T., Gohl O., Martinez-Arias R., Jacobi C., Starkuviene V., Schlenczeck S., Dencker S., Huber R., Klenk H.-P., Kramer W., Merkl R., Gottschalk G., Fritz H.-J.; "The genome sequence of the extreme thermophile Thermus
                                                                                                                                                         Grueter E.;
Thesis (2000), Department of Parasitology, Institute of Zoology,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.6%; Score 112; DB 2; Length 104; 38.3%; Pred. No. 1.9; tive 12; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                     Score 113; DB 2; Length 91;
Pred. No. 1.5;
2; Mismatches 35; Indels
                                                                                                                                                                                                                   STRAIN-STIB 755;
Grueter E., Betschart B.;
Grueter (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ287593; CAB76175.1; -.
SEQUENCE 91 AA; 9038 MW; A6CB89FIB3BA748D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104 AA; 11672 MW; A01FBCE249900B1F CRC64;
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6-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                72 AKAEKKEYAAAEAKKAEAAKA--YKAEAAKAAAKEA 105
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              91 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 AA
                                  Created)
             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                          Trypanosoma brucei gambiense
                                                                                                                                                                                                                                                                                       21.8%;
                                  01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    V-type ATPase subunit.
OrderedLocusNames=TTC0913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 38.33
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                            47; Conservative
             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=262724;
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STRAIN-STIB 755;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=15064768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thermophilus."
                                                                   Histone H1.
Name=H1A91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                       Query Match
           Q9NFJ9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukāryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 KKASPKKAAAKKASPKKAAAKK-ASPKKAAARKTAAKKTAKKPAVRKPAAKKRA-----
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PRINTS; PR00624; HISTONRHS.
Chromosomal protein; DNA-binding; Multigene family; Nuclear protein.
SEQUENCE 90 AA; 9236 MW; 899950A99D598D6C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95059220; PubMed=7969272; DOI=10.1016/0166-6851(94)90082-5;
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STRAIN=DC3000;
MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;
MEDLINE=22834015; PubMed=12928499; M., Selengut J., Paulsen I.T.,
Gwinn M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F.,
Madupu R., Daugherty S.C., Brinkac L.M., Beanan M.J., Haft D.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aaslund L., Carisson L., Henriksson J., Rydaaker M., Toro G.C., Galanti N., Pettersson U.,
"A gene family encoding heterogeneous histone H1 proteins in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas syringae (pv. tomato).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 KYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKE 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 24, Created)
(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
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72 AKAEKKEYAAAEAKKA-EAAKAYKAEAAKAAAKE 104
                                                                        68 ILARYRERAEAEAKAVREKAMARLDEAVALVLKE 101
                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                    PRT;
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01-FEB-1995 (Rel. 31, Last seq
01-NOV-1995 (Rel. 32, Last ann
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                                                                                                                                                                                                                                                                    STANDARD;
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01-MAR-2004 (TrEMBLre
Hypothetical protein.
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Trypanosoma cruzi.
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SEQUENCE
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Q26907;
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Matches
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         RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 KASAAPKKAVAKK---AAPKKAVAKKAAP--KKAVAKKAAPKKAVAKKAAPKKAVAKKAA 57
                                                                                                                                                                                                                                                                                                                                                                                                                    5 AKKAEKAYAKKAKAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEAYKAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 KYAKKAEKAYAKKAKAKEKKAYAKKEAKAYKAAEAKKKA--KAEAKKYAKEAAKAKKEA
Nelson W.C., Davidsen T.M., Zafar N., Zhou L., Liu J., Yuan Q., Khouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J., Utterback T.R., Van Aken S.E., Feldblyum T.V., D'Ascenzo M. Deng W.-L., Ramos A.R., Alfano J.R., Cartinhour S., Chatterjee A.K., Bender C.L., White O., Fraser C.M., Collmer A.; Bender C.L., White O., Fraser C.M., Collmer A.; Fraegrome sequence of the Arabidopsis and tomato pathogen Pseudomonas syringae pv. tomato DC3000."; Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186 (2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=H1C81; Synonyms=H1B81;
Trypanosoma brucei gambiense.
Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=31285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Grueter E.;
Thesis (2000), Department of Parasitology, Institute of Zoology,
                                                                                                                                                                                                                                                                                                                                                                          3;
                                                                                                                                                                                                                                                                                                                          21.1%; Score 109.5; DB 2; Length 82; 39.0%; Pred. No. 2.3; artive 16; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 109; DB 2; Length 81;
Pred. No. 2.4;
3; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SERVENCE FROM: N. 1257;
STRAIN-STIB 755, and 1257;
Grueter E., Betschart B.;
Grueter E., Betschart B.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ278460; CAB76178.1; -.
GO; GO:0000786; C:nucleosome; IEA.
GO; GO:00005634; C:nucleos; IEA.
GO; GO:0005634; C:nucleosis IEA.
GO; GO:0005634; P:nucleosome assembly; IEA.
INTERPO: IRR056319; Histone H5.
                                                                                                                                                                                                                                                        Complete proteome, Hypothetical protein.
SEQUENCE 82 AA; 8888 MW; 3826079839FAD75C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8012 MW; 3610C86DFDED5320 CRC64;
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 PKKAAPKKVAPKKVAGKK----AAAKKA 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 AKKYAKAAKAEKKEYAAAEAKK 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SKP-EKAKKSDKSEKAEKPAKK 80
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50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR005819; Histor
PRINTS; PR00624; HISTONEHS
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                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 32; Conserv
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Best Local Similarity
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29 EAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEAYKAEAKKYAKAKAKKEYAAAEAKKAE 88
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NCBL_TaxID=31285;
                                                                                                                                                                               Bukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae, Trypanosoma.
NCBL_TaxID=5693;
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDILINE-89364992; PubMed=2475776; DOI=10.1016/0166-6851(89)90115-1;
Lafaille J.J., Linss J., Krieger M.A., Souto-Padron T., de Souza W.,
Goldenberg S.;
                                                                                                                                                                                                                                                                                                                                                                                   "Structure and expression of two Trypanosoma cruzi genes encoding antigenic proteins bearing repetitive epitopes.";
MOI. Biochem. Parasitol. 35:127-136(1989).

EMBL; J04016; AAA3017.1; -.

Interpro; IPR009761; CRA_rpt.

MON MEN PF07046; CRA_rpt. 2.
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Thesis (2000), Department of Parasitology, Institute of Zoology,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 108.5; DB 2; Length 68;
Pred. No. 2.3;
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Pred. No. 2.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22; Indels
                                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 26, Last annotation update)
Cytoplasmic repetitive antigen (CRA) protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Grueter E., Betschart B.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
BMBJ, AJ272461; CAB76171.1; -.
GO; GO:0000786; C:nucleosome; IEA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0005674; F:DNA binding; IEA.
GO; GO:0006334; P:nucleosome assembly; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 AA; 7208 MW; ED6CF031B3DE7D1F CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Mismatches
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PRINTS; PR00624; HISTONEH5.
SEQUENCE 81 AA; 8040 MW; 3608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trypanosoma brucei gambiense.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20.9%;
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PRELIMINARY;
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Best Local Similarity
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Search completed: June 3, 2005, 11:52:52 Job time: 172 secs

Matches 47; Conservative 2; Mismatches 27; Indels 18; Gaps

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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June Run on:

3, 2005, 11:35:01 ; Search time 158 Seconds (without alignments) 266.816 Million cell updates/sec

US-10-792-311-7 519 Perfect score:

Sequence:

1 AKKYAKKAEKAYAKKAKAAK......AKAYKAEAAKAAAKEAAYEA 109

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

2105692 seqs, 386760381 residues Searched:

1202928 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 109

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

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A_Geneseq_16Dec04:* 1: geneseqp1980s:*

geneseqp2003as:* geneseqp2003bs:* geneseqp2002s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:*

geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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uo.	Copolymer	Copolymer	Copolymer	Copolymer	Recombina	Copolymer	Peptide #	Amino aci	Nucleic a	Poly-Lys-	Tumour ne	Peptide #	Amino aci	Nucleic a	Poly-L-Ly	Copolymer	Structura	Nucleatin	Structura	Nucleatin	Structura	Nucleatin	Structura	Nucleatin	Structura
Description	Aay82577	Aay82576	Aay82575	Aay82574	Aar06446	Aay82573	Aay98499	Aay59044	Aab45852	Aau04289	Abg71044	Aay98497	Aay59042	Aab45850	Aau04287	Aay82572	Ade10636	Adk15655	Ade10637	Adk15656	Ade10633	Adk15652	Ade10638	Adk15657	Ade10612
. di	AAY82577	AAY82576	AAY82575	AAY82574	AAR06446	AAY82573	AAY98499	AAY59044	AAB45852	AAU04289	ABG71044	AAY98497	AAY59042	AAB45850	AAU04287	AAY82572	ADE10636	ADK15655	ADE10637	ADK15656	ADE10633	ADK15652	ADE10638	ADK15657	ADE10612
DB	۳	٣	٣	ო	7	٣	٣	m	4	4	S	m	٣	4	4	٣	7	ω	7	œ	7	œ	7	œ	7
Length	109	98	77	99	106	26	100	100	100	100	80	100	100	100	100	45	105	105	106	106	104	104	106	106	98
% Query Match	100.0	60.2	55.7	44.0	36.0	34.8	34.6	34.6	34.6	34.6	28.2	27.2	27.2	27.2	27.2	26.6	25.9	25.9	25.9	25.9	25.7	25.7	25.0	25.0	24.9
Score	519	312.5	289	228.5	187	180.5	179.5	179.5	179.5	179.5	146.5	141	141	141	141	138	134.5	134.5	134.5	134.5	133.5	133.5	129.5	129.5	129
Result No.	-	7	ю	4	ī,	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22		24	25

Nucleatin	Structura	Nucleatin		Nucleatin	Structura	Nucleatin	Structura												
Adk15631	Ade10634	Adk15653	Ade10605	Adk15624	Ade10608	Adk15627	Ade10632	Adk15651	Ade10635	Adk15654	Ade10609	Adk15628	Ade10613	Adk15632	Ade10640	Adk15659	Ade10639	Adk15658	Ade10630
ADK15631	ADE10634	ADK15653	ADE10605	ADK15624	ADE10608	ADK15627	ADE10632	ADK15651	ADE10635	ADK15654	ADE10609	ADK15628	ADE10613	ADK15632	ADE10640	ADK15659	ADE10639	ADK15658	ADE10630
œ		80	7	æ	7	œ	7	œ	7	8	7	œ	7	œ	7	œ	7	œ	7
98	104	104	83	83	85	85	104	104	104	104	79	79	79	79	104	104	106	106	104
24.9	24.8	24.8	24.7	24.7	24.7	24.7	24.6	24.6	24.4	24.4	24.3	24.3	24.1	24.1	24.1	24.1	24.1	24.1	23.6
129	128.5	128.5	128	128	128	128	127.5	127.5	126.5	126.5	126	126	125	125	125	125	125	125	122.5
26	27	.28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; (Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus. Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:7. AAY82577 standard; peptide; 109 AA (first entry) 28-JUL-2000 AAY82577; RESULT 1 AAY8257 

Unidentified

WO200018794-A1.

06-APR-2000.

99WO-US022402. 24-SEP-1999; 98US-0101693P. 25-SEP-1998; (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA-IÑC.

Gad A, Lis D;

WPI; 2000-317499/27.

Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.

Claim 10; Page 14; 72pp; English.

AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and am amino acid composition corresponding to the copolymer. The polypeptides

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of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune thyroiditis, autoimmune thromboytopaenia purpura, collitis, contact sensitivity disease, diabetes mellitus, graves disease, Guillain-Barre's sensitivity disease, diabetes mellitus, graves disease, Guillain-Barre's
                                                                                                                                                                                                                       syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as molecular weight markers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AKKYAKKAEKAYAKKAKAKAKKKAYAKKEAKAYKAAEAKKKAKAKEAKKYAKEA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidabetic; thyromimetic; hemostetic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; crohn: a disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AKKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAKAEAKKYAKEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 YKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAKEAAYEA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 YKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAAYEA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 519; DB 3; Length 109; 100.0%; Pred. No. 4.1e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pemphigus vulgaris; systemic lupus erythematosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY82576 standard; peptide; 86 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 109 AA;
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which we consider the present specifically considered to the present invention. The present invention describes polypeptides (I) for determining the molecular weight and an an among of a copolymer (EP), which has an identified molecular weight and an an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatizamer of the invention are used as molecular weight markers for glatizamer to the invention are used as molecular weight markers for glatizamer acterated tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune harmolytic anaemia, autoimmune chyrodiditis, autoimmune thyrodiditis, autoimmune thyrodiditis, autoimmune thyrodiditis, contains, contact sensitivity disease, dispetes mellitus, Graves disease, Grillian-Barre's syndrome, Hashimoto's disease, dicipathic myxoedema, myaathenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated mediated diseases which can be treated include host-versus-graft disease, and delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to glatizamer acetate molecules, which mees them ideal for use as molecular weight markers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AKKYAKKAEKAYAKKAKAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKEA 60
                                                                      AAY82571 to AAY82577 represent specifically claimed copolymer molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 YKAEAKKYAKAAKAEKKEYAAAEAK-KAEAA-KAYKAEAAKAAAKEAAYEA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37 -KAEAKKYAKAAAKAEKKEYAAAEAKKAEAAKKAYKAEAAKAAYKAEAAKKAY 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60.2%; Score 312.5; DB 3; Length 86; 72.1%; Pred. No. 5.3e-19; ive 1; Mismatches 3; Indels 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pemphigus vulgaris; systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY82575 standard; peptide; 77 AA.
                       Claim 10; Page 14; 72pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 86 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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(YEDA ) YEDA RES & DEV CO LTD.

Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.

WPI; 2000-317499/27.

Gad A, Lis D;

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Weight TV-marker polypeptides from the present invention. The present invention describes polypeptides [1] for determining the molecular weight TV-marker polypeptides [1] for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatizamer of the invention are used as molecular weight markers for glatizamer treated terrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune haemolytic anaemia, autoimmune chrombocytopaenia purpura, collitis, contact sensitivity disease, chronic immune thrombocytopaenia purpura, collitis, contact sensitivity disease, dispetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, psoriated diseases which can be treated include host-versus-graft disease, graft-versus-nost disease, and delayed-type hypersenaitivity. The molyperides of the invention have defined molecular weights and physical
                                                                                                                                                                      Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as molecular weight markers
                                                                                                                                                                                                                                                         Claim 10; Page 14; 72pp; English.
(TEVA-) TEVA PHARM USA INC
                                                                                                                WPI; 2000-317499/27
                                                           Gad A,
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Sequence 77 AA;

1 AKKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEA 60 3; Indels 32; Gaps 1 AKKYAKK-EKAYAKKA-----EKAAKKAEAKAYKAAEAKKKA-----61 YKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAAYEA 109 - KAEAKKYAKAAKAEKKEYAAAEAK - - - - - YKAEAKAAAKEAAYEA 77 Score 289; DB 3; Length 77; Pred. No. 4.3e-17; 1; Mismatches 3; Indels 55.7%; 73; Conservative Query Match Best Local Similarity Matches 73; Conserva ò

AAY82574 standard; peptide; 66 AA. AAY82574;

28-JUL-2000 (first entry)

Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:4.

Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; antianmatory condition; multiple sclerosis; rheumatoid arthritis; crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus 

Jnidentified

WO200018794-A1.

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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an expense of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases such diseases include either cell-mediated or antibody-mediated diseases such diseases include either cell-mediated or antibody-mediated diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune cophoritis, autoimmune thyroididis, euchommune uveoretinitis, Contact arthritis, osteoarthritis, autoimmune bamolytic anaemia, autoimmune cophoritis, autoimmune thyroidmine weightes, contact sensitivity disease, disease, idiopathic mysoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, osteoatis, pemphigus vulgaris, osteoate, idiopathic mysoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated mediated disease, which are analogous to glatiramer acetate molecules, which are analogous to glatiramer acetate molecules, which makes them ideal for use as molecular weight markers
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                                                                                                                                                                                                                                                                                                                       Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 YKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAAYEA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 - KAEAKKYAKAAKAEKKEYAAAEAK - - - - - YKAEAAKAAAKEAAYEA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.0%; Score 228.5; DB 3; Length 66; 56.9%; Pred. No. 4e-12; ive 0; Mismatches 4; Indels 4:
                                                                                                                                                                                                                                                                                                                                                                                                Claim 10; Page 14; 72pp; English
                                                                                                                                                         (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.
                                                               99WO-US022402.
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Matches 62; Conservative
                                                                                                                                                                                                                                                                             WPI; 2000-317499/27.
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                                                                                                                                                                                                                               3ad A, Lis D;
                                                                                                             25-SEP-1998;
                                                                    24-SEP-1999;
                     06-APR-2000
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AAR06446 standard; protein; 106 AA (revised) 25-MAR-2003 03-JAN-1991 AAR06446; 

Recombinant copolymer 1-19, myelin basic profein analogue.

(first entry)

Recombinant copolymer 1; COP-1-19; myelin basic protein; MBP; immunological activity; autoimmune encephalomyelitis; multiple sclerosis.

Synthetic.

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Transporter system; nucleic acid delivery; gene therapy; cancer;
 pemphigus vulgaris; systemic lupus erythematosus.
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                                                                                                                                                                                                                                                                                                                                              To improve the expression of rCOP-1 polypeptides in E. coli, genes coding for rCOP-1-19 were subcloned from pREV 2.1 to pBG3-2deltaN (deposit: 20-NOV-1984 US4691009), NREL B-15910), a plasmid used to express Protein A. The resulting plasmids encode fusion proteins consisting of beta-cocurs between the Protein A, and rCOP-1 sequences. A methionine residue cocurs between the Protein A and rCOP-1 sequences, originating from the cocurs between the Protein A and rCOP-1 sequences, originating from the cocurs between the Protein. TCOP-1 sequences, originating from the cocurs between the Protein. TCOP-1 sequences, originating from the cocurs between the Protein. TCOP-1 polypeptide may be cleaved from the fusion protein. TCOP-1-19 contains oligonucleotide duplexes incoding the following segments: YKK, AAE, KAK, EKA, YEA, AKA KEA, and AAA. The N-terminal alamine residue is left behind following CNBr cleavage of the fusion protein. The product prevents or arrests experimental autoimmune encephalomyelitis. They are used to prevent, arrest or control a demyelinating disorder, e.g. multiple sclerosis. They are also be used as additives to hair care products to confer beneficial effects on damaged hair or as supplements for diets deficient in certain effects on damaged hair or as supplements for diets deficient in certain and adminisher the product of the correct PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                  Producing genes encoding random polymers of aminoacid(s) - for producing recombinant polypeptide(s) with biological and/or immunological activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antidanemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; crohn's disease; ohronic immune thrombocyropaenia purpura; colitis; diabetes mellitus; Graves disease; duillain.Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AKAAEKAKAAK-KAYEAEKAKAKYEAK--KAEKAEKAEKAEKAKKAKEAKKAEK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20; Indels 18; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 AKKYAKAAKAEKKEYAAAEAKKAEAA----KAYKAEAAKAAAK-EAAYE 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Copolymer; molecular weight marker; TV-marker; immune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 36.0%; Score 187; DB 2; Length 106; 1 Similarity 55.0%; Pred. No. 1.9e-08; 60; Conservative 11; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                    Disclosure, Fig 12; 25pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY82573 standard; peptide; 56 AA
                                                                 90EP-00301700
                                                                                               89US-00312541.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-JUL-2000 (first entry)
                                                                                                                                              (REPK ) REPLIGEN CORP.
                                                                                                                                                                                                                 WPI; 1990-255848/34.
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Best Local Similarity
Matches 60: Conserv
                                                                                                                                                                                                                                   N-PSDB; AAQ06446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 106 AA;
                                                                16-FEB-1990;
                                                                                                                07-FEB-1990;
                                                                                                 17-FEB-1989;
                                22-AUG-1990
EP383620-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY82573;
                                                                                                                                                                                  Cook KS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY82573
윤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ~$&$$$$$$$$$$$$$$
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AAY82571 to AAY82577 represent specifically claimed copolymer molecular weight TV-marker polypeptides (1) for determining the molecular weight invention describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an coff composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatizamer actetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases of treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases such inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic ansemia, autoimmune cophoritis, autoimmune thyroidmune haemolytic ansemia, autoimmune cophoritis, autoimmune thyroidmune uveoretninis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myscedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated mediated diseases which can be treated include host-versus-graft disease, or graft-versus-host disease, and delayed-type hypersensitivity. The properties which are analogous to glatizamer acetate molecules, which makes them ideal for use as molecular weight markers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AKKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKBAAKAKKEA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34.8%; Score 180.5; DB 3; Length 56; 45.9%; Pred. No. 3.4e-08; cive 3; Mismatches 3; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide #10 used in nucleic acid transporter system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY98499 standard; peptide; 100 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 10; Page 14; 72pp; English
                                                                                                                                                                                                                                                                                                                                                                                                       E.
                                                                                                                                                                                                                                                                                                                       98US-0101693P.
                                                                                                                                                                                                                                           99WO-US022402.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   (YEDA ) YEDA RES & DEV
(TEVA-) TEVA PHARM USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-317499/27.
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Best Local Similarity
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                                                                           WO200018794-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sad A, Lis D;
Unidentified.
                                                                                                                                                                                                                                   24-SEP-1999;
                                                                                                                                                                                                                                                                                                                       25-SEP-1998;
                                                                                                                                                           36-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY98499;
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39

Location/Qualifiers 3. .100 /note= "Lys-Ala in positions 3 to 100 may be optionally absent"

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Nucleic acid transport system, useful for creating transgenic animals for assessing human disease such as cancer in an animal model.
              Key
Misc-difference
The present invention relates to a transporter system for delivering nucleic acid to a cell. The system comprises a nucleic acid binding complex, consisting of a binding molecule bonded non-covalently to the nucleic acid, and covalently to a surface ligand, and alytic agent. The binding molecule is apermine or a spermidine derivative. Nucleotide sequences AAA3663-A36652 and peptide sequences AAV38456-Y98500 are used the construction of the transporter system of the invention. The transporter system is used in gene therapy, particularly to deliver nucleic acids to hepatocytes, muscle cells or bone forming cells, e.g for transportar disease, cancer, and infection. The transporter systems are also used to create transpent animals (as models for human carcinogenesis or disease or for drug testing). Other uses include transforming cells to produce proteins, or transfecting cells in vitro to study the function of the nucleic acid. The use of a surface ligand allows specific targeting of selected cells and tissues. The lytic agent provides for release of the nucleic acid into the cellular interior, from
                                                                                                                                                                                                                                                                 System for transporting nucleic acid into cells, useful e.g. in gene therapy and for generating transgenic animals, comprises binding agent linked to nucleic acid, surface ligand and lytic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               endosomes, without requiring endosomal or lysosomal degradation
                                                                                                                                                                                                            Smith LC;
carcinogenesis; cardiovascular disease; infection.
                                                                                                                                                                                                            WOO SLC,
                                                                                                                                                                                                                                                                                                                         Disclosure; Col 125-128; 108pp; English.
                                                                                                                                                                                                           Cristiano RJ,
                                                                                                                                                                               (BAYU ) BAYLOR COLLEGE MEDICINE
                                                                                                                                      92US-00855389.
93WO-US002725.
                                                                                                            93US-00167641.
                                                                                                                                                                                                                                        WPI; 2000-281993/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence 100 AA;
                                                                                                                                                                                                            Sottchalk S,
                                                                                                            14-DEC-1993;
                                                                                                                                      20-MAR-1992;
19-MAR-1993;
                                                       US6033884-A
                                                                                 07-MAR-2000
                           Synthetic.
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Smith LC

Sparrow J,

SLC, Cristiano RJ, Gottchalk S,

WPI; 2000-038262/03.

(BAYU ) BAYLOR COLLEGE MEDICINE

92US-00855389. 93WO-US002725. 93US-00167641.

95US-00460890

03-JUN-1995; 20-MAR-1992; 14-DEC-1993;

30-NOV-1999

US5994109-A

Disclosure; Col 123-124; 107pp; English.

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The invention relates to a nucleic acid transport system (NTS) for delivering nucleic acid into a cell. The NTS contains but is not limited to 5 components: (a) the nucleic acid or a macromolecule to be delivered; (b) a moiety that recognizes and binds to a cell surface receptor or antigen or is capable of entering a cell through cytosis; (c) a nucleic acid or macromolecular molecule binding moiety; (d) a moiety that is capable of moving or initiating movement through a nuclear membrane; and/or (e) a lysis moiety that enables the transport of the entire complex from the cell surface directly into the cytoplasm of the cell. The NTS delivers nucleic acid into the cellular interior as well as the nucleus of specific cells. The NTS can be used to treat disorders by targeting specific nucleic acid accordingly. The NTS can also be used to create transgenic animals for assessing human disease, such as cencer, in an animal model. The NTS can be used in vitro with tissue culture cells. The NTS can be used in vitro with tissue culture cells. The NTS can be used in vitro with tissue culture cells. The NTS can be used in vitro with tissue culture cells. The NTS can be used in vitro with tissue culture cells. The NTS can be used in vitro with tissue culture cells. The NTS can be used in vitro with tissue culture cells. The NTS can be used in vitro with tissue culture cells. The NTS can be setted tissue culture cells. The ADD contract of the problem of endosomal/lysosomal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 KKAEKAYAK-KAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKEAYKAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 3; Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid transporter system peptide ligand SEQ ID NO 64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 AKKYAKA-AKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAK 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34.6%; Score 179.5; DB 3
55.0%; Pred. No. 7.6e-08;
tive 8; Mismatches 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB45852 standard; protein; 100 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 100 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB45852;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
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3; Gaps

34.6%; Score 179.5; DB 3; Length 100; 55.0%; Pred. No. 7.6e-08; tive 8; Mismatches 34; Indels 3.

Local Similarity 55.0 nes 55; Conservative

Query Match

65 AKKYAKA-AKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAK 103 

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Nucleic acid transport system; NTS; cell surface receptor; cytosis; nuclear membrane; lysis moiety; transgenic animal; human disease; nucleic acid delivery; cancer.

Synthetic

Amino acid polymer seq ID NO: 64 of US5994109.

(first entry)

07-MAR-2000

AAY59044;

AAY59044 standard; peptide; 100

RESULT 8

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The sequence represents poly-lys-Ala, used to bind nucleic acid in a nucleic acid transporter system. The nucleic acid transporter system uses nucleic acid binding complexes containing surface ligands which are capable of binding to a cell surface receptor and entering the cell through cytosis. The compounds of the invention are either ligands, binding molecules (surface ligands), lysis agents, spacer molecules or their intermediates. The ligands, binding molecules, lysis agents and spacer molecules are used in nucleic acid transporter systems to deliver nucleic acid into specific cells e.g. in gene therapy to deliver nucleic acid into hepatocytes, muscle cells or bone forming cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid transport system, useful for creating transgenic animals for assessing human disease such as cancer in an animal model.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 KKAEKAYAK-KAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEAYKAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumour necangiogenesis, peptidase substrate; tumour related disorder; tumour-selective intravascular coagulation inducing molecule; blood clotting; tumour vascularisation; tumour growth control;

    ..100
/note= "Lya-Ala in positions 3-100 may be present or
absent"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34.6%; Score 179.5; DB 4; Length 100; 55.0%; Pred. No. 7.6e-08; Live 8; Mismatches 34; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 AKKYAKA-AKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAK 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gottchalk S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ...crence 9. .16 /note= "Optionally absent" Misc-difference 17. .24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Col 131; 111pp; English.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                          Cristiano RJ,
                                                                                                                                                                                                                                                                                                                             BAYU ) BAYLOR COLLEGE MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG71044 standard; peptide; 80
                                                                                                                                                                                                                                       92US-00855389.
93WO-US002725.
93US-00167641.
                                                                                                                                                                                                95US-00462040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 55.0
les 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                heparin-binding peptide.
                                                                                                                                                                                                                                                                                                                                                                        Smith LC,
                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-365933/38
                    Misc-difference 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 100 AA;
                                                                                                                                                                                                                                           20-MAR-1992;
19-MAR-1993;
                                                                                                                                                                                                05-JUN-1995;
                                                                                                                                                                                                                                                                                      14-DEC-1993;
                                                                                                          US6177554-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-DEC-2002
                                                                                                                                                     23-JAN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to a cell, comprising a binding complex comprising a ligand binding molecule noncovalently bound to a nucleic acid and covalently linked to a surface ligand, and a second binding complex comprising a second binding molecule noncovalently bound to a nucleic acid and covalently linked to a nuclear ligand. The complexes are simultaneously bound to the nucleic acid transporter system can also be used in method for the invivo targeting of the insertion of DNA into a cell. It can system can be used in processes for producing transformed cell lines. The system can be used to deliver a variety or proteins and polypeptides, such as hormones, growth factors, arbitry or proteins and polypeptides, apolipoproteins, receptors, drugs, oncogenes, tumor antigens, tumor antigens, tumor appressors, viral antigens, parasitic antigens, and bacterial antigens. The transporter system uses lysis agents to overcome the problems of endosomal/lysosomal degradation seen with prior art systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel system (I) for delivering a nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ce]],
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid transport; cytosis; ligand; lysis agent; spacer molecule; gene therapy; hepatocyte; muscle; bone forming cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 KKAEKAYAK-KAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEAYKAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   useful for delivering proteins and polypeptides to cells, including growth factors, enzymes, hormones, and tumor suppressors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid transporter system for delivering nucleic acid into a
tumor antigen; tumor suppressor; viral antigen; parasitic antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 100;
                                                                                                                                                                                                                                                                                                                                                                        WOO SLC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 AKKYAKA-AKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAK 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Poly-Lys-Ala used in nucleic acid transporter system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith LC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34.6%; Score 179.5; DB 4;
55.0%; Pred. No. 7.6e-08;
iive 8; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                      Cristiano RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Col 125-126; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU04289 standard; peptide; 100 AA
                                                                                                                                                                                                                                                                                                                           (BAYU ) BAYLOR COLLEGE MEDICINE
                                                                                                                                                                                                                                     92US-00855389.
93WO-US002725.
93US-00167641.
                                                                                                                                                                                                95US-00460971.
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                                                                                                                                                                                                                                                                                                                                                                        Sparrow J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-049093/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 55; Conserv
                        bacterial antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 100 AA;
                                                                                                                                                                                                                                                                                                                                                                        Gottchalk S,
                                                               Unidentified
                                                                                                                                                                                                                                                              19-MAR-1993;
14-DEC-1993;
                                                                                                                                                                                              05-JUN-1995;
                                                                                                        JS6150168-A
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                                                                                                                                                   21-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU04289
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AAU04289
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XSXXXXXXXXXXXX

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64

Gaps

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93US-00167641.
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Best Local Similarity
                                                                                                                                                       WPI; 2000-281993/24.
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 100 AA;
                                                                                                                                   Gottchalk S,
                                                            14-DEC-1993;
                                                                                0-MAR-1992;
                                                                                           19-MAR-1993;
                   US6033884-A
                                        07-MAR-2000
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY59042;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        manufacture of a medicament for the treatment and/or prevention of tumour related disorders. The compounds are able to induce blood clotting at tumour sites resulting in the disruption of the tumour vaccularisation and consequently in the control of tumour growth. This sequence represents a heparin-binding peptide, a postively charged polymer that can be incorporated into a substrate for extracellular hydrolases
                                                                                                                                                                                                                                                                                                                New tumor-selective intravascular coagulation inducing molecules useful
                                                                                                                                                                                                                                                                                                                                                                             the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 KKAEKAYAKKAKAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKEAYKAEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 KKAAKAARKKAARARKKA----AKAAR----KKAAKAARKKAAKAARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25; Gaps
                                                                                                                                                                                                                                                                                                                                                                 The invention describes tumour-selective intravascular coagulation inducing molecules. The molecules are useful as a medicine and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transporter system; nucleic acid delivery; gene therapy; cancer; carcinogenesis; cardiovascular disease; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28.2%; Score 146.5; DB 5; Length 80; 46.5%; Pred. No. 3.4e-05; Live 9; Mismatches 20; Indels 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     releasable by tumour or neoangiogenic endothelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 KKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----KAAKAARKK--AAKAARKKAAKAAKKAAKAA 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide #8 used in nucleic acid transporter system
                                                                                                      55. .72
'note= "Optionally absent"
'3. .80
       25. .32
/note= "Optionally absent"
                                              .48
.e= "Optionally absent"
                                                                    49. .56 /note= "Optionally absent"
                                                                                         57. .64
/note= "Optionally absent"
                                                                                                                                             /note= "Optionally absent"
"Optionally absent"
                            33. .40
/note= "Optionally absent"
                                                                                                                                                                                                                                                                                                                                             Claim 20; Page 27; 40pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY98497 standard; peptide; 100
                                                                                                                                                                                                                                                  (UYLO-) UNIV CATHOLIQUE LOUVAIN.
                                                                                                                                                                                                                               30-JAN-2001; 2001EP-00870017.
                                                                                                                                                                                                          30-JAN-2002; 2002WO-EP000951.
                                                                                                                                                                                                                                                                                                                           control of tumor growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-JUL-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47; Conservative
/note=
25. .32
                                                            /note=
                                                                                                                                                                                                                                                                       Frouet A, Dubois V;
                                                                                                             disc-difference 65.
                                                                                                                                                                                                                                                                                           WPI; 2002-706887/76.
                                                  Misc-difference 41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                          Misc-difference 57
                             Misc-difference 33
                                                                                                                                   Misc-difference 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 80 AA;
                                                                                                                                                                  NO200260488-A1
                                                                                                                                                                                     08-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY98497;
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Matches
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The present invention relates to a transporter system for delivering mucleic acid to a cell. The system comprises a nucleic acid binding complex, consisting of a binding molecule bonded non-covalently to the nucleic acid, and covalently to a surface ligand, and a lytic agent. The binding molecule is spermine or a spermidine derivative. Nucleotide squences AAA36633-AA3652 and peptide sequences AAA98456-Y98500 are used in the construction of the transporter system of the invention. The transporter system is used in gene therapy, particularly to deliver uncleic acids to hepatocytes, muscle cells or bone forming cells, e.g for treating cardiovascular disease, cancer, and infection. The transporter systems are also used to create transgenic animals (as models for human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 carcinogenesis or disease or for drug testing). Other uses include transforming cells to produce proteins, or transfecting cells in vitro or study the function of the nucleic acid. The use of a surface ligand allows specific targeting of selected cells and tissues. The lytic agent provides for release of the nucleic acid into the cellular interior, from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KKYAKKAEKAYAKKAKAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEAY 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      System for transporting nucleic acid into cells, useful e.g. in gene therapy and for generating transgenic animals, comprises binding agent linked to nucleic acid, surface ligand and lytic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid transport system; NTS; cell surface receptor; cytosis; nuclear membrane; lysis moiety; transgenic animal; human disease; nucleic acid delivery; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   endosomes, without requiring endosomal or lysosomal degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                     Smith LC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 KAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAK 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WOO SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.2%; Score 141; DB 3; 37.8%; Pred. No. 0.00012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amino acid polymer seq ID NO: 62 of US5994109.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13; Mismatches
                                                                                                                                                                                                     Cristiano RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Col 125-126; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY59042 standard; peptide; 100 AA
                                                                                                                 (BAYU ) BAYLOR COLLEGE MEDICINE
92US-00855389.
93WO-US002725.
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                                                                                                                                                                                                         Sparrow J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37; Conservative
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92US-00855389. 93WO-US002725. 93US-00167641.

20-MAR-1992; 19-MAR-1993; 14-DEC-1993;

95US-00460971

05-JUN-1995;

Unidentified.

US6150168-A. 21-NOV-2000

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The invention relates to a nucleic acid transport system (NTS) for delivering nucleic acid into a cell. The NTS contains but is not limited to 5 components: (a) the nucleic acid or a macromolecule to be delivered; (b) a moiety that recognizes and binds to a cell surface receptor or antigen or is capable of entering a cell through cytosis; (c) a nucleic acid or macromolecular molecule binding moiety; (d) a moiety that is capable of moving or initiating movement through a nuclear membrane; and/or (e) a lysis moiety that enables the transport of the entire complex from the cells unface directly into the cytoplasm of the cell. The NTS delivers nucleic acid into the cellular interior as well as the nucleus of specific nucleic acid accordingly. The NTS can also be used to create transgenic animals for assessing human disease, such as cancer, in an animal model. The NTS can be used in vitro with tissue culture cells which allows the role of various nucleic acids to be studied by targeting specific expression into specifically targeted tissue culture cells. The lysis agent within the NTS avoids the problem of endosomal/lysosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                              Nucleic acid transport system, useful for creating transgenic animals for assessing human disease such as cancer in an animal model.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid delivery; nucleic acid transporter system; hormone; enzyme; growth factor; clotting factor; apolipoprotein; receptor; drug; oncogene; tumor antigen; tumor suppressor; viral antigen; parasitic antigen; bacterial antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 KKYAKKAEKAYAKKAKAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKEAY 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                /note= "Lys in positions 3 to 100 may be optionally
                                                                                                                                                                                                                                                                                          Smith LC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid transporter system peptide ligand SEQ ID NO 62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.2%; Score 141; DB 3; Length 100; 37.8%; Pred. No. 0.00012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 KAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAK 99
                                                                                                                                                                                                                                                                                        Gottchalk S, Sparrow J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Col 121-122; 107pp; English.
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                                                                                                                                                                                                                                                     (BAYU ) BAYLOR COLLEGE MEDICINE
                                                                                                                                                                                                93WO-US002725.
93US-00167641.
                                                                                                                                             95US-00460890.
                                                                                                                                                                               92US-00855389
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                                 absent"
                                                                                                                                                                                                                                                                                        Cristiano RJ,
.100
                                                                                                                                                                                                                                                                                                                          WPI; 2000-038262/03
Misc-difference 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 100 AA;
                                                                                                                                             03-JUN-1995;
                                                                                                                                                                                                  19-MAR-1993;
14-DEC-1993;
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                                                                                                         30-NOV-1999
                                                                       US5994109-A
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WWW.XEXEXEX.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                to a cell, comprising a binding complex comprising a ligad binding molecule noncovalently bound to a nucleic acid and covalently linked to a surface ligand, and a second binding complex comprising a second binding molecule noncovalently bound to a nucleic acid and covalently linked to a nuclear ligand. The complexes are simultaneously bound to the nucleic acid. The nucleic as system can also be used in a method for the in vivo targeting of the insertion of DNA into a cell. It can also be used in processes for producing transformed cell lines. The system can be used to deliver a variety or proteins and polypeptides, apolipoproteins, receptors, drugs, oncogenes, tumor antigens, tumor suppressors, viral antigens, parasitic antigens, and bacterial antigens. The transporter system uses lysis agents to overcome the problems of endosomal/lysosomal degradation seen with prior art systems
                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes a novel system (I) for delivering a nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid transporter system for delivering nucleic acid into a cell, useful for delivering proteins and polypeptides to cells, including growth factors, enzymes, hormones, and tumor suppressors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid transport, cytosis; ligand; lysis agent; spacer molecule; gene therapy; hepatocyte; muscle; bone forming cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 KKYAKKAEKAYAKKAKAKAKEKKAYAKKEAKAYKAAEAKKKKAKAEAKKYAKEAAKAKKEAY
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                                                                                                                                                                                                                                                           WOO SLC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27.2%; Score 141; DB 4; Length 100; 37.8%; Pred. No. 0.00012; ive 13; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Poly-L-Lysine used in nucleic acid transporter system.
                                                                                                                                                                                                                                                             Smith LC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 KAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAK
                                                                                                                                                                                                                                                             Gottchalk S, Sparrow J, Cristiano RJ,
                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Col 123-124; 105pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU04287 standard; peptide; 100 AA.
                                                                                                                                                                                                                          (BAYU ) BAYLOR COLLEGE MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 37.8 es 37; Conservative
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Misc-difference 3. .100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 100 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU04287;
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The sequence represents poly-L-lysine, used to bind nucleic acid in a nucleic acid transporter system. The nucleic acid transporter system uses nucleic acid binding complexes containing surface ligands which are capable of binding to a cell surface receptor and entering the cell through cytosis. The compounds of the invention are either ligands, binding molecules (surface ligands), lysis agents, spacer molecules or their intermediates. The ligands, binding molecules, lysis agents and spacer molecules are used in nucleic acid transporter systems to deliver nucleic acid into specific cells e.g. in gene therapy to deliver nucleic acid into hepatocytes, muscle cells or bone forming cells
                                                                                                                                                                                                                                                                                                               Nucleic acid transport system, useful for creating transgenic animals for assessing human disease such as cancer in an animal model.
/note= "Lys in positions 3-100 may be present or absent"
                                                                                                                                                                                                                                              Sparrow J;
                                                                                                                                                                                                                                              Gottchalk S,
                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Col 129; 111pp; English.
                                                                                                                                                                                                                                              Smith LC, Cristiano RJ,
                                                                                                                                                                                                         (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                                                    92US-00855389.
93WO-US002725.
93US-00167641.
                                                                                                     95US-00462040.
                                                                                                                                                                                                                                                                                WPI; 2001-365933/38.
                                                                                                                                      20-MAR-1992;
19-MAR-1993;
14-DEC-1993;
                                US6177554-B1
                                                                                                    05-JUN-1995;
                                                                   23-JAN-2001
                                                                                                                                                                                                                                              WOO SLC,
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2 KKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKEAY 61 0; Gaps Query Match

27.2%; Score 141; DB 4; Length 100;
Best Local Similarity 37.8%; Pred. No. 0.00012;
Matches 37; Conservative 13; Mismatches 48; Indels 셤 ઠે

Sequence 100 AA;

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62 KAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAK 99

8

Search completed: June 3, 2005, 11:49:54 Job time : 159 secs

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3, 2005, 11:53:02; Search time 138 Seconds (without alignments) 273.037 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                              1465611 seqs, 345679903 residues
                                                                                OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum Match 100
                                                                                                                                                                                                  US-10-792-311-7
519
                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0 Maximum DB seq length: 109
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                                                                                                                                                                                                                                                                                   Scoring table:
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                                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                                                                 Searched:
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                                                                                                                      Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 7, Appli	Sequence 7, Appli	Sequence 6, Appli	Sequence 6, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 3, Appli	Seguence 3, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 43, Appl
SUMMARIES	ΩI	US-09-816-989A-7	US-10-792-311-7	US-09-816-989A-6	US-10-792-311-6	US-09-816-989A-5	US-10-792-311-5	US-09-816-989A-4	US-10-792-311-4	US-09-816-989A-3	US-10-792-311-3	US-09-816-989A-2	US-10-792-311-2	US-10-177-725-43
	DB	6	17	σ	17	σ	17	σ	17	0	17	σ	17	14
	Query Match Length DB	109	109	98	98	77	77	99	99	26	26	45	45	105
de	Query	100.0	100.0	60.2	60.2	55.7	55.7	44.0	44.0	34.8	34.8	26.6	26.6	25.9
	Score	519	519	312.5	312.5	289	289	228.5	228.5	180.5	180.5	138	138	134.5
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43,	44,	44,	40,	40,					41,	41,	12,	12,	15,	15,						16,	20,	20,	47,	47,	46,	46,	37,	37,	51,	51,	38,	
Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	
Ä		-10-393-449-4	US-10-177-725-40	-10-393-449-4	-10-177-725-4	-10-393-449-4	- 1	-10-393-449-1	-10-177-725-4	-10-393-449-4	-10-177-725-1	-10-393-449-1	US-10-177-725-15	-10 - 393 - 449 - 1	-10-177-725-3	-10-393-449-3	-10-177-725-4	US-10-393-449-42	US-10-177-725-16	US-10-393-449-16	US-10-177-725-20	US-10-393-449-20	US-10-177-725-47	-10-393-449-4	-10-177-725-4	-10-393-449-4	US-10-177-725-37	-10-393-449-3	-10-177-725	93-449	-10-177-725-3	ALIGNMENTS
15	14	15	14	15	14	15	14	15	14	15	14	15	14	15	14	15	14	15	14	15	14	15	14	15	14	15	14	15	14	15	14	
105	106	106	104	104	106	106	98	98	104	104	83	83	82	82	104	104	104	104	79	79	79	79	104	104	106	106	104	104	91	91	104	
25.9	25.9	25.9	25.7	25.7	25.0	25.0	24.9	24.9	24.8	24.8	24.7	24.7	24.7	24.7	24.6	24.6	24.4	24.4	24.3	24.3	24.1	24.1	24.1	24.1	24.1	24.1	23.6	23.6	23.5	23.5	23.5	
134.5	134.5	134.5	133.5	133.5	129.5	129.5	129	129	128.5	128.5	128	128	128	128	127.5	127.5	126.5	126.5	126	126	125	125	125	125	125	125	122.5	a	122	122	122	
14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

## ALIGNMENTS

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| Sequence 7, Application US/0981698A
| Patent No. US20020115103A1
| GENERAL No. US20020115103A1
| GENERAL No. US20020115103A1
| APPLICANT: Gad, Alexander | APPLICANT: Lis, Doris | APPLICANT: COPOLYMER | RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKE | TITLE OF INVENTION: AND FOR THERAPEUTIC USE | TITLE OF INVENTION: AND FOR THERAPEUTIC USE | CURRENT FILING DATE: 2004-03-23 | PRIOR PELICATION NUMBER: 60/101,693 | PRIOR PILING DATE: 1998-09-24 | NUMBER OF SEQ ID NOS: 7 | SOFTWARE: Patentin Version 3.1 | SEQ ID NOS: 7 | SOFTWARE: Patentin Version 3.1 | SEQ ID NOS: 7 | SOFTWARE: Patentin Version 3.1 | SEQ ID NOS: 7 | SOFTWARE: Patentin Version 3.1 | SEQ ID NOS: 7 | SEQ ID NOS: 7 | SEQ ID NOS: 7 | SEC ID NOS: 7 |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AKKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEA
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llarity 100.0%; Pred. No. 8.8e-34;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
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Matches 109; Conserv
JS-09-816-989A-7
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APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKE
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKE
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REPERENCE: 2609/60807-A-PCT-US
CURRENT PELING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR FILING DATE: 1999-09-24
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKI
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT PILING DATE: 2004-03-02
RIOR APPLICATION NUMBER: US/9/816,989
PRIOR FILING DATE: 2001-03-23
PRIOR FILING DATE: 2001-03-23
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1999-09-24
                           1 AKKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-10-792-311-6
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                                                          1 AKKYAKK-EKAYAKKA----EKAAKAEAKAYKAAEAKKKA

1 AKKYAKK-EKAYAKKA----EKAAKAEAKAYKAAEAKKKA
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Pred. No. 1.1e-17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/09816989A Patent No. US20020115103A1
                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/10792311 Publication No. US20050038233A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
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SOFTWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 77
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Best Local Similarity 72.1
Matches 80; Conservative
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APPLICANT: Gad, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gad, Alexander
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US-09-816-989A-5
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US-10-792-311-6
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APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFRERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/10/792,311
CURRENT PILING DATE: 2004-03-02
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO 7
LENGTH: 109
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TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION WUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 6
LENGTH: 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-10-792-311-7
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61 YKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAAYEA 109
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1. Similarity 72.1%; Pred. No. 1.1e-17;
80; Conservative 1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 519; DB 17;
Pred. No. 8.8e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/09816989A Patent No. US20020115103A1 GENERAL INFORMATION:
                                                                                                                            Sequence 7, Application US/10792311
Publication No. US20050038233A1
GENERAL INFORMATION:
APPLICANT: Gad, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%;
Best Local Similarity 100.0%;
Matches 109; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gad, Alexander
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Matches 80; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-816-989A-6
                                                                                                         JS-10-792-311-7
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TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKA TITLE OF INVENTION: AND FOR THERAPEUTIC USE FILE REPERENCE: 2609/60807-A-PCT-US CURRENT APPLICATION NUMBER: US/10/792,311

CURRENT APPLICATION NUMBER: US/09/816,989

PRIOR PLILING DATE: 2001-03-23

PRIOR PLILING DATE: 2001-03-23

PRIOR PLILING DATE: 1999-09-25

PRIOR PLILING DATE: 1999-09-25

PRIOR PLILING DATE: 1999-09-24
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APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKI
                                                                                                                                                                                                                                                                                                                                                                                                1 AKKYAKKAEKAYAKKAKAKAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AKKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEA 60
                                                                                                                                                                                                           ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-10-792-311-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43;
                                                                                                                                                                                                                                                                                                                                                 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 YKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAAYEA 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26 -KAEAKKYAKAAKAEKKEYAAAEAK-----YKAEAAKAAAKEAAYEA 66
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Pred. No. 3.1e-11;
0; Mismatches 4; Indels 43
                                                                                                                                                                                                                                                                                          DB 9; Length 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AKKYAKK-EKAYAKKA------EAKAAKKA---
                                                                                                                                                                                                                                                                                        Score 228.5; DB 9
Pred. No. 3.1e-11;
                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09816989A Patent No. US20020115103A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/10792311; Publication No. US20050038233A1; GENERAL INFORMATION:
                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                     ch 44.0%;
1 Similarity 56.9%;
62; Conservative
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SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 56.9%;
Matches 62; Conservative
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                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 62; Conserva
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                                                                            SEQ ID NO 4
LENGTH: 66
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CURRENT PILING DATE: 2004-03-02
RRIOR APPLICATION NUMBER: US/09/816,989
PRIOR FILING DATE: 1901-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR FILING DATE: 1998-09-25
RRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VERSION 3.1
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TITLE OF INVENTION: AND FOR THERAPEUTIC USE
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                                                                                                                                                                                                           1 AKKYAKKAEKAYAKKAKAKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEA 60
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                        ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-10-792-311-5
                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                   61 YKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAAYEA 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 55.7%; Score 289; DB 17; Length 77; Best Local Similarity 67.0%; Pred. No. 6.6e-16; Matches 73; Conservative 1; Mismatches 3; Indels
                                                                                                     Length 77;
                                                                                                                                                         3; Indels
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                                                                                                                                                                                                                                         55.7%; Score 289; DB 9;
67.0%; Pred. No. 6.6e-16;
tive 1; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                    - KAEAKKYAKAAKAEKKEYAAAEAK-
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Patent No. US20020115103A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/10792311
Publication No. US20050038233A1
GENERAL INFORMATION:
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                                                                                                                                 Best Local Similarity 67.03
Matches 73; Conservative
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APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Gad, Alexander
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                                                                                                           Query Match
  FEATURE:
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APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKE
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REPERBACE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR APPLICATION NUMBER: PCT/US99/22402
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PALENT IN OS: 7
SOFTWARE: PALENT IN OS: 7
LENGTH 45
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TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKI
TITLE OF INVENTION: AND FOR THERABEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989
FRIOR APPLICATION NUMBER: 08/09/816,989
FRIOR APPLICATION NUMBER: 60/101,693
FRIOR FILING DATE: 2001-03-25
FRIOR FILING DATE: 1998-09-25
FRIOR FILING DATE: 1998-09-25
FRIOR FILING DATE: 1999-09-24
NUMBER: PATCH STATE ST
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-10-792-311-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 26.6%; Score 138; DB 9; Length 45; Best Local Similarity 76.6%; Pred. No. 0.00026; Matches 36; Conservative 0; Mismatches 7; Indels
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                                                    Sequence 2, Application US/09816989A
Patent No. US20020115103A1
GENERAL INFORMATION:
APPLICANT: Gad, Alexander
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Publication No. US20050038233A1
GENERAL INFORMATION:
APPLICANT: Gad, Alexander
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ORGANISM: Artificial Sequence
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                US-09-816-989A-2
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US-10-177-725-43
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; Sequence 3, Application US/10792311
; Publication No. US20050038233A1
; GENERAL INFORMATION:
    APPLICANT: Add, Alexander
; APPLICANT: Lis, Doris
; TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
; TITLE OF INVENTION: AND FOR THERAPEUTIC USE
; TITLE OF INVENTION NUMBER: US/10/792,311
; CURRENT APPLICATION NUMBER: US/09/816,989
; PRIOR APPLICATION NUMBER: 60/101,693
; PRIOR FILLING DATE: 1999-09-25
; PRIOR FILLING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 7
; SEQ ID NO 3
; SEQ ID NO 3
; LENGTH: 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53; Gaps
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34.8%; Score 180.5; DB 17; Length 56;
Best Local Similarity 45.9%; Pred. No. 1.5e-07;
Matches 50; Conservative 3; Mismatches 53; Indels 53
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FILLE OF INVENTION: AND FOR THERAPEUTIC USE
CURRENT APPLICATION NUMBER: US(9)/816,989A
CURRENT FILING DATE: 2001-03-23
FRIOR FILING DATE: 2001-03-23
FRIOR APPLICATION NUMBER: 60/101,693
FRIOR FILING DATE: 1998-09-25
FRIOR APPLICATION NUMBER: PCT/US99/22402
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PALCHIN VERSION 3.1
SEQ ID NO 3
LENGTH: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
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US-10-792-311-3
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APPLICANT: Anderson, David
APPLICANT: Anderson, David
APPLICANT: Bogenberger, Jakob M.
APPLICANT: Bogenberger, Jakob M.
APPLICANT: Peele, Ream R.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT SC
FILE REFERENCE: A-66900-4/RMS/AMS
CURRENT APPLICATION NUMBER: US 09/415,765
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR PILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 173
SOFTWARE: PatentIn version 3.1
SEQ ID NO 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 AAKEKKAYAKKEAKAYKAAEAKKKAKAEA----KKYAKEAAKAKCEAYKAEAKKYAKAAK 73
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  74 AEKKEYAAAEAKKAEAAKAYKAEAAKAAKEAAYEA 109
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                                Search completed: June 3, 2005, 12:05:53
Job time : 139 secs
                                                                                                                                                                      US-10-177-725-44
; Sequence 44, Application US/10177725
; Publication No. US20030143562A1
; GENERAL INFORMATION:
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ORGANISM: Artificial sequence
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Sequence 43, Application US/10393449

Sequence 43, Application World US20030224412A1

Sequence 43, Application No. US20030224412A1

Sequence 43, Application No. US20030224412A1

SERNERAL INFORMATION:
APPLICANT: Begenberger, Jakob M.
APPLICANT: Begenberger, Jakob M.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT FILE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT FILE OF INVENTION NUMBER: US/10/393,449

CURRENT PILING DATE: 2003-03-18

PRIOR APPLICATION NUMBER: US 09/415,765

PRIOR PILING DATE: 1999-10-08

PRIOR FILING DATE: 1999-10-08

NUMBER OF SEQ ID NOS: 173

SOFTHARE: PATENTING VARIANCE OF SEQ ID NOS: 173

SEQ ID NO 43

LENGTH: 105
                                   GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Anderson, David
APPLICANT: Bogenberger, Jakob M.
APPLICANT: Bele, Beau R.
TITLE OF INVENTION: STRUCTURALLY BIASED RANDOM PEPTIDE LIBRARIES BASED ON DIFFERENT (FILE REFERENCE: A-66900-4/RMS/AMS
CURRENT APPLICATION NUMBER: US/01/17,725
CURRENT FILING DATE: 1999-10-08
PRIOR APPLICATION NUMBER: US 09/415,765
PRIOR APPLICATION NUMBER: US 09/169,015
PRIOR PILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 173
SOFTWARE: PeacentIn version 3.1
SEQ ID NO 43
LENGTH: 105
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Sequence 43, Application US/10177725
Publication No. US20030143562A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial sequence
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COTHER INFORMATION: synthetic
US-10-177-725-43
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RESULT 2
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LENGTH: 109
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                                                                                                                                1 AKKYAKKAEKAYAKKAKAAK......AKAYKAEAAKAAKEAAYEA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
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/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-107-532A-6743
US-08-993-008A-5
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US-09-816-989A-6
US-09-405-743A-5
US-09-405-743A-4
US-09-405-743A-4
US-09-816-989A-4
US-09-816-989A-4
US-08-816-989A-4
US-08-860-890A-64
US-08-460-890A-64
US-08-460-890A-62
US-08-460-890A-62
US-08-460-871A-62
US-08-460-871A-62
US-08-460-871A-62
US-08-460-871A-62
US-08-460-871A-62
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US-08-460-871A-62
US-09-405-743A-2
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                                                                                                                                                                                       513545 seqs, 74649064 residues
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                                                                                                                                                                                                                                                                                           Listing first 45 summaries
                                            OM protein - protein search, using sw model
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Match Length DB
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519
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28 110.5 21.3 60 1 US-08-246-849-16 Sequence 16, Appl 20 110.5 21.3 60 2 US-08-293-284A-16 Sequence 16, Appl 30 110.5 21.3 60 4 US-08-898-300-16 Sequence 16, Appl 31 110.5 21.3 60 4 US-08-898-300-16 Sequence 16, Appl 32 10.6 2.0 Sequence 20, Appl 33 10.6 20.8 68-255-9 Sequence 9, Appl 34 105 20.2 35 4 US-09-816-989A-1 Sequence 2, Appl 36 104.5 20.1 61 US-08-868-251-9 Sequence 1, Appl 37 104.5 20.1 61 US-08-898-310-17 Sequence 17, Appl 39 104.5 20.1 61 US-08-898-310-17 Sequence 17, Appl 39 104.5 20.1 61 US-08-898-310-17 Sequence 17, Appl 40 103 19.8 100 3 US-08-460-800A-63 Sequence 63, Appl 41 103 19.8 100 3 US-08-460-907A-63 Sequence 63, Appl 44 102 19.7 103 19.8 100 3 US-08-460-907A-63 Sequence 63, Appl 44 102 19.7 103 US-08-462-040-63 Sequence 34, Appl 45 19.2 19.7 103 US-08-462-040-63 Sequence 36, Appl 45 19.2 19.7 103 US-08-462-040-63 Sequence 16642, Appl 45 19.2 19.3 US-08-462-040-63 Sequence 16642, Appl 45 19.3 US-08-462-040-63 Sequence 16642, Appl 45 19.3 US-08-462-040-63 Sequence 16642, Appl 46 19.2 19.7 US-08-902-2640-16642
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Sequence 7. Application US/09816989A

Sequence No. 6800287

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: COPOLYMER I RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKE
TITLE OF INVENTION: APPLICANTION: AND FOR THERAPEUTIC USE
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
CURRENT APPLICATION NUMBER: US/09/816,989A

CURRENT FILING DATE: 1998-09-25

PRIOR FILING DATE: 1998-09-25

PRIOR PPLING DATE: 1999-09-24
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Sequence 7, Application US/09405743A
Patent No. 6514938
GENERAL INFORMATION:
APPLICANT: Yeda Research and Development Co., Ltd.
APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: G12AIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REPERENCE: 60807-A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ IO NOS: 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 YKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAAKBAKBAYKA 109
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; OTHER INFORMATION: PEPTIDE
US-09-405-743A-7
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100.0%; Pred. No. 7.7e-37;
tive 0; Mismatches 0;
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Matches 109; Conservative
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Gaps

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TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKET TITLE OF INVENTION: AND FOR THERAPEUTIC USE TITLE OF INVENTION: AND FOR THERAPEUTIC USE CURRENT APPLICATION NUMBER: US/09/816,989A CURRENT PILING DATE: 2001-03-23 PRIOR APPLICATION NUMBER: 60/101,693 PRIOR FILING DATE: 1998-09-25 PRIOR APPLICATION NUMBER: PCT/US99/22402 PRIOR FILING DATE: 1999-09-24
                                                                                                                                                                                                                                                                                                                                                              1 AKKYAKKAEKAYAKKAKAKAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKKKEA 60
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                                                                                                                                                                          ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-6
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Patent No. 6514938
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Yea Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS FILE REFERENCE: 60807-A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                         Score 312.5; DB 4;
Pred. No. 1.1e-19;
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Pred. No. 8.8e-18;
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APPLICANT: Gad, Alexander APPLICANT: Lis, Doris
                          PatentIn version 3.1
                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 72.1%;
Matches 80; Conservative
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Best Local Similarity 67.00
Best Local 3; Conservative
  NUMBER OF SEQ ID NOS: 7
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US-09-405-743A-5
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                          SOFTWARE: Pat
SEQ ID NO 6
LENGTH: 86
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LENGTH: 77
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                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
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TITLE OF INVENTION: GLOGIAA
FILE REPERBENCE: 60807-A
CURRENT REPERBENCE: 60807-A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT PILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 2.1
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                       Query Match 100.0%; Score 519; DB 4; Length 109; Best Local Similarity 100.0%; Pred. No. 7.7e-37; Matches 109; Conservative 0; Mismatches 0; Indels
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NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO 7
                                                                                                       TYPE: PRT ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 72.17
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LENGTH: 86
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Gaps

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POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKE
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                                                                                                                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-4
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TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                          Score 228.5; DB 4; Length 66;
Pred. No. 8.6e-13;
0; Mismatches 4; Indels 4
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34.8%; Score 180.5; DB 4; Length 56;
Best Local Similarity 45.9%; Pred. No. 7.4e-09;
Matches 50; Conservative 3; Mismatches 3; Indels 5:
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; Patent No. 6800287
; GENERAL INFORMATION:
    APPLICANT: Gad, Alexander
; APPLICANT: Lis, Doris
    TITLE OF INVENTION: AND FOR THERAPEUTIC USE
; FILE REFERENCE: 2609/60807-A-FCT-US
; CURRENT APPLICATION NUMBER: 05/09/816,989A
; CRRENT FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/22402
; PRIOR APPLICATION NUMBER: PCT/US99/22402
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     NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 66
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Best Local Similarity 56.9%;
Matches 62; Conservative
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US-09-816-989A-3
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LENGTH: 56
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Sequence 4. Application US/09816989A

GENERAL INCORMATION:
GENERAL INCORMATION:
APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERABEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: 06/101,693
PRIOR APPLICATION NUMBER: PCT/US99.22402
PRIOR FILING DATE: 1999-09-24
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TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REPERENCE: 60807-A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SEGTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 66
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Pred. No. 8.8e-18;
1; Mismatches 3; Indels
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NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 77
                                                                                                                                                                                                                                                                            Query Match 55.7%;
Best Local Similarity 67.0%;
Matches 73; Conservative 1
                                                                                                                                            ORGANISM: Artificial Sequence
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US-09-816-989A-4
                                                                                                                     TYPE: PRT
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CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
             TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
US-08-167-641C-64
                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AKKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAKAEAKKYAKEAAKO
                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide US-09-816-989A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 YKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAAYEA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----YKAEAAKAAKEAAYEA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AKKYAKK-EKAYAKKA----EKAAKKAEAKAYKAAEAKKKAEAK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APELICANT: Woo, Savio L.C.
APELICANT: Smith, Louis C.
APELICANT: Smith, Louis C.
APELICANT: Cristiano, Richano, Richand, Richard, Richard,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 34.8%; Score 180.5; DB 4; Best Local Similarity 45.9%; Pred. No. 7.4e-09; Matches 50; Conservative 3; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Lyon & Lyon
STREET: 633 West Pifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READMBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARGATA AFFLICATION NUMBER: US/08/460,890A
FILING DATE: June 5, 1995
CLASSIFICATION NATA:
PRIOR APPLICATION NATA:
APPLICATION NUMBER: 08/167,641
FILING DATE: December 14, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: 07/893/02725
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg Richard J.
REGISTRATION NUMBER: 32,327
REGECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
TELEFAX: (213) 955-0440
TELEFAX: 67.3510
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: FastSEQ for Windows 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 64, Application US/08460890A
Patent No. 5994109
GENERAL INFORMATION:
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 56
                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 100 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
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6 KKAEKAYAK-KAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEAYKAE 64
                                                                                                                                                                                                               Gaps
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Patent No. 6033884

GENERAL INFORMATION:
APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: MUCLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: 631 West Fifth Street
                                                                                                                                                       ch 34.6%; Score 179.5; DB 2; Length 100; 1 Similarity 55.0%; Pred. No. 1.6e-08; 55; Conservative 8; Mismatches 34; Indels 3
                                                   OTHER INFORMATION: "Lys Ala" in positions 3 to 100 may be OTHER INFORMATION: present or absent.

US-08-460-890A-64
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                                                                                                                                                                                                                                                                                                                                                                    65 AKKYAKA-AKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAK 103
                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastERG for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/167,641C
FILING DATE: December 14, 1993
CLASSIFICATION: 435
PRIOR APPLICATION ATA:
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US33/02725
FILING DATE: March 19, 1993
ATTONNEY, FAGENT INFORMATION:
NAME: WARDING, RICHARD A.C. REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 205/012
TELECHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 100 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
MOLECULE TYPE: peptide FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
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Gaps

34; Indels

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6 KKAEKAYAK-KAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEAYKAE 64
                                                                                              65 AKKYAKA-AKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAK 103
                                                                                                                                                                                                         60 AKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAK 99
Best Local Similarity 55.0%; Pred. No. 1.6e-08;
Matches 55; Conservative 8; Mismatches 34
                                                                                                                                                                                                                                                                                                       US-08-462-040-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                       6 KKAEKAYAK-KAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEAYKAE 64
                                                                                                                                                               Gaps
                                                                                            3;
                                         Query Match
34.6%; Score 179.5; DB 3; Length 100;
Best Local Similarity 55.0%; Pred. No. 1.6e-08;
Matches 55; Conservative 8; Mismatches 34; Indels 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: MUCLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: "Lys Ala" in positions 3 to 100 may ; OTHER INFORMATION: present or absent.
                                                                                                                                                                                                                              65 AKKYAKA-AKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAK 103
                                                                                                                                                                                                                                                         60 akakakakakakakakakakakakakakaky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: TESTS OF OF WINDOWS 2.0
SOFTWARE: FASTS OF OF WINDOWS 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,971A
FILING DATE: June 5, 1995
CLASSIFICATION DATE: WS/08/460,971A
FILING DATE: December 14, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 19, 1993
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: WARDING RICHARD J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 212/063
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                      US-08-460-971A-64; Sequence 64, Application US/08460971A; Patent No. 6150168; GENERAL INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 100 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
US-08-167-641C-64
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34.6%; Score 179.5; DB 3; Length 100;

Query Match

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M
                                                                  APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Smith, Louis C.
APPLICANT: Smith, Louis C.
APPLICANT: Gristiano, Richard J.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.6%; Score 179.5; DB 3; Length 100; 55.0%; Pred. No. 1.6e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: "Lys Ala" in positions 3 to 100 may be OTHER INFORMATION: present or absent.

US-08-462-040-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compactible
COMPUTER: IBM Compactible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEG for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,040
FILING DATE: UNDES, 1995
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/167,641
FILING DATE: December 14, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US93/02725
APPLICATION NUMBER: PCT/US93/02725
APPLICATION NUMBER: PCT/US93/02725
ATTONNEY/AGENT INPORMATION:
NAME: WALDING, RICHART J.
                                                                                                                                                                                                                                                                                                                                                        CITY: Los Angeles
STARE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 212/078
TELECOMMUNICATION INFORMATION:
Sequence 64, Application US/08462040
Patent No. 6177554
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 64
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 100 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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6 KKAEKAYAK-KAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKEAYKAE 64
                          0; Gaps
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US-08-460-890A-62
                                                                                                                                                                                                                                       Sequence 62, Application US/08460890A; Sequence 62, Application US/08460890A; Patent No. 5994109; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Woo, Savio L.C.
APPLICANT: Gritiano, Richard J.
APPLICANT: Gritiano, Richard J.
APPLICANT: Gottchalk, Stephen; TTLE OF INVENTION: METHODS OF USE
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65;
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48; Indels
                                                                                          65 AKKYAKA-AKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAK 103
                                                                                                                  60 akakakakakakakakakakakakakakaky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 27.2%; Score 141; DB 2; Best Local Similarity 37.8%; Pred. No. 2.6e-05; Matches 37; Conservative 13; Mismatches 48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTENG for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,890A
FILING DATE: June 5, 1995
CLASSITICATION: 435
PRICATION NUMBER: 08/167,641
FILING APPLICATION DATA:
APPLICATION NUMBER: 08/167,641
FILING DATE: March 19, 1993
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 19, 1993
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REFERENCE/DOCKET NUMBER: 212/066
TELEFRA: 67-3510
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: TELEFRASS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
COMPTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Lyon & Lyon
633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide FEATURE:
                                                                                                                                                                                                                             US-08-460-890A-62
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Search completed: June 3, 2005, 11:54:24 Job time: 43 secs